GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 21, 2004, 02:05:42 ; Search time 11154 Seconds
(without alignments)
11391.904 Million cell updates/sec

Title: US-09-900-751-1
Perfect score: 3106
Sequence: 1 catggtagacggctgcccgg.....ttaaaaaaaaaaaaaaaaaa 3106

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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1: gb_ba:*
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37: em_htg_vrt:*
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39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3106	100.0	3106	6	AX395268	AX395268 Sequence
2	3106	100.0	3106	10	AF042822	AF042822 Mus muscu
3	3102.8	99.9	3248	10	BC005496	BC005496 Mus muscu
4	2595	83.5	3174	10	AB049189	AB049189 Rattus no
5	2313.6	74.5	2568	10	AB037898	AB037898 Rattus no
6	1905.6	61.4	3273	9	BC030532	BC030532 Homo sapi
7	1889.8	60.8	3149	9	AF118224	AF118224 Homo sapi
8	1884.8	60.7	3120	9	AF133086	AF133086 Homo sapi
9	1884.6	60.7	3128	9	AB030036	AB030036 Homo sapi
10	1883.2	60.6	3147	6	AR081724	AR081724 Sequence
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c 12	1883.2	60.6	3147	6	AR229712	AR229712 Sequence
13	1883.2	60.6	3147	6	AX207897	AX207897 Sequence
14	1883.2	60.6	3147	6	AX207945	AX207945 Sequence
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16	1530.8	49.3	2900	6	AR081725	AR081725 Sequence
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18	1530.8	49.3	2900	9	HSU20428	U20428 Human SNC19
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22	701.2	22.6	1553	6	AR263832	AR263832 Sequence
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38	239.2	7.7	1327	6	AX538208	AX538208 Sequence
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40	239.2	7.7	3143	6	AX538206	AX538206 Sequence
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c 43	212.2	6.8	182736	2	AC021672	AC021672 Homo sapi
44	212.2	6.8	190314	9	AC019227	AC019227 Homo sapi
45	206	6.6	734	6	AX375702	AX375702 Sequence

ALIGNMENTS

RESULT 1
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LOCUS AX395268 3106 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 5 from Patent WO0203787.
ACCESSION AX395268
VERSION AX395268.1 GI:21066293
KEYWORDS .
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Allen,K.D. and Leviten,M.W.
TITLE Transgenic mice containing targeted gene disruptions
JOURNAL Patent: WO 0203787-A 5 17-JAN-2002;

Deltagen, Inc. (US)

FEATURES Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"

BASE COUNT 692 a 862 c 897 g 655 t

ORIGIN

Query Match 100.0%; Score 3106; DB 6; Length 3106;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION  Mus musculus epithin mRNA, complete cds.
ACCESSION   AF042822
VERSION     AF042822.3  GI:7330637
KEYWORDS    .
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  AUTHORS   Kim,M.G., Chen,C., Lyu,M.S., Cho,E.G., Park,D., Kozak,C. and
            Schwartz,R.H.
  TITLE     Cloning and chromosomal mapping of a gene isolated from thymic
            stromal cells encoding a new mouse type II membrane serine
            protease, epithin, containing four LDL receptor modules and two CUB
            domains
  JOURNAL   Immunogenetics 49 (5), 420-428 (1999)
  MEDLINE   99216440
   PUBMED   10199918
REFERENCE   2  (bases 1 to 3106)
  AUTHORS   Kim,M.G., Chen,C., Cho,E., Park,D. and Schwartz,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-JAN-1998) Laboratory of Cellular and Molecular
            Immunology, NIAID, NIH, 9000 Rockville Pike, Bethesda, MD 20892,
            USA
REFERENCE   3  (bases 1 to 3106)
  AUTHORS   Kim,M.G., Chen,C., Cho,E., Park,D. and Schwartz,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-1999) Laboratory of Cellular and Molecular
            Immunology, NIAID, NIH, 9000 Rockville Pike, Bethesda, MD 20892,
            USA
  REMARK    Sequence update by submitter
REFERENCE   4  (bases 1 to 3106)
  AUTHORS   Kim,M.G., Chen,C., Cho,E., Park,D. and Schwartz,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-MAR-2000) Laboratory of Cellular and Molecular
            Immunology, NIAID, NIH, 9000 Rockville Pike, Bethesda, MD 20892,
            USA
  REMARK    Sequence update by submitter
COMMENT     On Mar 27, 2000 this sequence version replaced gi:6435480.
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RESULT 3
BC005496
LOCUS       BC005496               3248 bp    mRNA    linear   ROD 16-APR-2003
DEFINITION  Mus musculus suppression of tumorigenicity 14 (colon carcinoma),
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ACCESSION   BC005496
VERSION     BC005496.1  GI:13529565
KEYWORDS    MGC.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
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  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
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  TITLE     Generation and initial analysis of more than 15,000 full-length
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2  (bases 1 to 3248)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-MAR-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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ORIGIN
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Query Match 99.9%; Score 3102.8; DB 10; Length 3248;
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RESULT 4
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ACCESSION   AB049189
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REFERENCE   1  (sites)
  AUTHORS   Inoue,H., Takahashi,K. and Kishi,K.
  TITLE     membrane-bound arginine specific serine protease
  JOURNAL   Published Only in DataBase (2000)
REFERENCE   2  (bases 1 to 3174)
  AUTHORS   Inoue,H., Takahashi,K. and Kishi,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-SEP-2000) Hideshi Inoue, Tokyo University of Pharmacy
            and Life Science, School of Life Science; 1432-1 Horinouchi,
            Hachioji-shi, Tokyo 192-0392, Japan (E-mail:hinoue@ls.toyaku.ac.jp,
            Tel:81-426-76-7153, Fax:81-426-76-7157)
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Qy       1261 ACTATGTGGAGATCAACGGGGAGAAGTACTGCGGTGAGAGGTCCCAGTTTGTGGTGAGCA 1320
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db       1325 ACTATGTGGAGATCAACGGGGAGAAGTTCTGCGGTGAGAGGTCCCAGTTTGTGGTGAGCA 1384

Qy       1321 GCAACAGCAGCAAGATTACAGTCCACTTCCATTCTGATCACTCGTACACGGACACCGGGT 1380
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db       1385 GCAACAGCAGCAAGATTACGGTCCACTTCCATTCTGATCACTCGTACACGGACACCGGGT 1444

Qy       1381 TCCTAGCTGAGTACCTCTCCTACGACTCCAACGACCCGTGCCCAGGGATGTTCATGTGCA 1440
              |||| |||||||| |||||||||||||||||||| ||||| |||||||||||||||| |
Db       1445 TCCTGGCTGAGTATCTCTCCTACGACTCCAATGACCCATGCCCAGGGATGTTCATGTGTA 1504

Qy       1441 AGACTGGACGGTGCATCCGAAAGGAACTGCGCTGCGACGGCTGGGCAGACTGCCCGGATT 1500
              |||||||||||||||||| ||||| |||||||||| |||||||| |||||||||| | |
Db       1505 AGACTGGACGGTGCATCCGCAAGGACTTGCGCTGCGATGGCTGGGCTGACTGCCCGGACT 1564

Qy       1501 ATAGTGATGAGCGTTACTGCCGATGCAATGCCACCCACCAGTTCACGTGCAAAAACCAGT 1560
              | |||||||||||| |||||||||||||| || |||||||||||| |||||| |||||||
Db       1565 ACAGTGATGAGCGTCACTGCCGATGCAACGCTACCCACCAGTTCATGTGCAAGAACCAGT 1624

Qy       1561 TCTGCAAGCCCCTCTTCTGGGTCTGTGACAGTGTCAACGACTGTGGGGACGGAAGTGACG 1620
              |||||||||||||||||||||||||||||||||||||||||||||||| || || | |||
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Qy       1621 AGGAGGGCTGCAGCTGTCCTGCTGGGAGTTTCAAGTGTTCCAATGGGAAGTGTCTCCCTC 1680
              |||||||||||| |||||||| |||||||||||||||||||||||||||||||||||||
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Qy       1681 AGAGCCAGAAGTGTAATGGGAAGGACAACTGTGGAGATGGGTCTGACGAGGCTTCATGTG 1740
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Db       1745 AGAGCCAGCAGTGTAATGGGAAGGACGACTGTGGAGATGGGTCTGACGAGGCCTCATGTG 1804
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Qy      1741 ACAGCGTGAATGTCGTCTCTTGCACCAAATATACCTACCGCTGCCAAAATGGCCTCTGTC 1800
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Qy      1801 TGAGCAAGGGCAACCCTGAGTGTGATGGGAAGACGGACTGTAGCGATGGCTCCGATGAGA 1860
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Qy      1861 AAAACTGTGACTGTGGGCTGCGATCCTTTACCAAACAGGCTCGCGTGGTTGGTGGCACGA 1920
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Qy      1921 ATGCGGACGAGGGCGAGTGGCCCTGGCAGGTGAGCCTCCACGCCCTGGGCCAGGGCCACT 1980
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Qy      2101 ACCAGAGCAAGCGCAGTGCCTCTGGGGTGCAGGAGCTGAAGCTCAAACGTATCATCACCC 2160
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Qy      2161 ACCCTTCCTTCAATGATTTCACCTTCGACTATGACATCGCCTTGCTGGAGCTGGAGAAGT 2220
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Qy      2221 CGGTGGAGTACAGCACCGTCGTGCGCCCCATCTGCCTGCCTGATGCTACCCATGTCTTCC 2280
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Qy      2281 CTGCTGGCAAGGCCATCTGGGTCACAGGCTGGGGGCACACAAAAGAGGGAGGTACCGGAG 2340
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Db      2345 CTGCCGGCAAAGCCATCTGGGTCACAGGCTGGGGCCACACGAAAGAAGGAGGAACTGGAG 2404

Qy      2341 CGCTGATCCTGCAGAAGGGTGAGATCCGTGTCATCAACCAGACCACCTGTGAGGACCTCA 2400
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Qy      2461 CCTGCCAGGGTGACTCTGGTGGCCCCCTTGTCAAGCGCGGAGAAAGATGGGCGAATGTTCC 2520
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Db      2525 CCTGCCAGGGTGATTCCGGTGGCCCCTTGTCCAGTGTGGAGAAAGATGGGCGAATCTTCC 2584

Qy      2521 AGGCTGGTGTGGTGAGCTGGGGTGAAGGCTGCGCTCAGAGGAACAAGCCAGGCGTGTACA 2580
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Qy      2641 AGACAGCCGACCACAAACACCCACAGGGATGCCCGACATGCACACCTGGATACAGGAGAG 2700
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Qy      2812 AGAGAGAACTTGCGTGCTAGCGGCCCAGCCTG----GGGGCAAGGGTTTGATGGCAGCCT 2867
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Qy      2868 TCCCCCTCTAGCCCTGAGCTGGGTGAAGATGATGCTGTCCCGGAGAGCTGCTTCC----- 2922
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Qy      2923 ---------AACTGTCATTGAGCTCCCGGGAGCCCTATGGGAGGAGGGGCTCAGGGTCAC 2973
                      |||| || | | ||||| ||| |||||||||  |||||||   ||
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Qy      2974 TCTTTTCAGGAAGCGCCAGCCCTAGGAACCCCAGAAAAGAGTGGTACCTAAGGCTGAAAT 3033
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Qy      3034 TGTTTTGCTGTTGCCAGGGGTGGGTATTTGAGAGTAAAACATTTTATTTCTTTTTAAAAA 3093
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Qy      3094 AAAAAAAAAAAAA 3106
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Db      3162 AAAAAAAAAAAAA 3174
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RESULT 5
AB037898
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DEFINITION  Rattus norvegicus MBSP mRNA for membrane bound serine protease,
            complete cds.
ACCESSION   AB037898
VERSION     AB037898.1  GI:9650963
KEYWORDS    membrane bound serine protease; MT-SP1.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1
  AUTHORS   Satomi,S., Yamasaki,Y., Tsuzuki,S., Hitomi,Y., Iwanaga,T. and
            Fushiki,T.
  TITLE     A role for membrane-type serine protease (MT-SP1) in intestinal
            epithelial turnover
  JOURNAL   Biochem. Biophys. Res. Commun. 287 (4), 995-1002 (2001)
  MEDLINE   21458307
   PUBMED   11573963
REFERENCE   2  (bases 1 to 2568)
  AUTHORS   Tsuzuki,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-JAN-2000) Satoshi Tsuzuki, Kyoto University, Graduate
            School of Agriculture, Division of Food Science and Biotechnology,
            Laboratory of Nutrition Chemistry; Oiwake-cho, Kitashirakawa,
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            (E-mail:tkmone@kais.kais.kyoto-u.ac.jp, Tel:81-75-753-6263,
            Fax:81-75-753-6264)
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                     /sex="male"
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                     /dev_stage="8 weeks old"
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                     /gene="MBSP"
     CDS             1. .2568
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                     /db_xref="GI:9650964"
                     /translation="MGNNRGRKAGGGSQDFGAGLKYNSRLENMNGFEEGVEFLPVNNA
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                IPPHLEEEVDRAMAVERVVTLPPRARALKSFVLTSVVAFPIDPRMLQRTQDNSCSFAL
                HARGRTVTRFTTPGFPNSPYPAHARCQWVLRGDADSVLSLTFRSFDVAPCDGHDSDLV
                TVYDSLSPMEPHAVVRLCGTFSPSYNLTFLSSQNVFLVTLITNTDRRHPGFEATFFQL
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BASE COUNT      559 a    708 c    746 g    555 t
ORIGIN

  Query Match            74.5%;  Score 2313.6;  DB 10;  Length 2568;
  Best Local Similarity  93.8%;  Pred. No. 0;
  Matches 2409;  Conservative    0;  Mismatches  159;  Indels    0;  Gaps    0;

Qy         63 ATGGGTAGCAATCGGGGCCGCAAGGCCGGAGGGGGCTCTCAGGACTTCGGCGCGGGACTC 122
Db          1 ATGGGGAACAATCGGGGCCGCAAGGCCGGAGGGGGCTCGCAGGACTTCGGCGCCGGACTC 60

Qy        123 AAGTACAACTCCCGGCTAGAGAACATGAATGGCTTTGAGGAGGGTGTGGAGTTCCTGCCT 182
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Qy        183 GCGAACAATGCCAAGAAAGTGGAGAAGCGAGGCCCCAGGCGCTGGGTGGTGCTGGTGGCA 242
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Qy        243 GTGCTGTTCAGCTTCCTCTTGCTCTCCCTCATGGCTGGCTTGCTGGTGTGGCACTTCCAT 302
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Db        241 TACCGGAATGTGAGGATCCAAAAGGTCTTCAATGGCCATCTGAGGATCACGAATGAGAAC 300

Qy        363 TTTCTGGATGCGTATGAGAACTCCACCTCCACAGAGTTTATCAGCCTGGCCAGCCAGGTG 422
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Qy        423 AAGGAGGCGCTGAAGCTGCTGTACAATGAAGTCCCTGTCCTGGGTCCCTACCACAAGAAG 482
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Qy        483 TCGGCTGTAACTGCCTTCAGTGAGGGCAGTGTCATCGCCTACTACTGGTCAGAGTTCAGC 542
Db        421 TCGACTGTAACTGCCTTCAGTGAGGGCAGCGTCATTGCCTACTACTGGTCAGAGTTCAGC 480

Qy        543 ATCCCCCCACACCTGGCAGAAGAGGTTGATCGCGCCATGGCTGTGGAGCGAGTTGTAACA 602
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Qy        603 TTGCCACCCCGAGCACGGGCACTGAAATCCTTCGTGCTAACATCTGTGGTGGCCTTCCCC 662
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Qy        723 CATGGTGCAGCAGTGACACGCTTCACTACCCCTGGCTTCCCCAACAGTCCCTACCCGGCG 782
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Qy        783 CATGCCCGCTGCCAGTGGGTCCTGCGGGGGGACGCCGACTCTGTGCTGAGCCTCACCTTC 842
Db        721 CATGCCCGCTGCCAGTGGGTCCTGCGGGGGGACGCGGACTCTGTGCTGAGCCTCACCTTC 780

Qy        843 CGAAGCTTTGATGTCGCTCCCTGTGATGAGCATGGCAGTGACCTGGTCACCGTGTATGAT 902
Db        781 CGAAGTTTTGATGTCGCGCCCTGTGATGGGCATGACAGTGACCTGGTCACAGTGTATGAC 840

Qy        903 AGCCTGAGCCCCATGGAACCCCACGCTGTGGTGCGGCTGTGTGGCACCTTCTCACCCTCC 962
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Qy        963 TACAACCTGACTTTCCTCTCCTCCCAGAACGTCTTCCTTGTCACGCTGATAACCAATACT 1022
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Qy       1023 GACCGGCGACATCCTGGCTTTGAGGCCACTTTCTTCCAGCTGCCCAAGATGAGCAGCTGT 1082
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Qy       1623 GAGGGCTGCAGCTGTCCTGCTGGGAGTTTCAAGTGTTCCAATGGGAAGTGTCTCCCTCAG 1682
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Qy       2403 CCGCAGCAGATCACCCCACGAATGATGTGTGTGGGTTTCCTCAGTGGGGGTGTGGACTCC 2462

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Qy       2463 TGCCAGGGTGACTCTGGTGGCCCCTTGTCAAGCGCGGAGAAAGATGGGCGAATGTTCCAG 2522

Db       2401 TGCCAGGGTGATTCCGGTGGCCCCTTGTCCAGTGTGGAGAAAGATGGGCGAATCTTCCAG 2460

Qy       2523 GCTGGTGTGGTGAGCTGGGGTGAAGGCTGCGCTCAGAGGAACAAGCCAGGCGTGTACACA 2582

Db       2461 GCTGGTGTGGTGAGCTGGGGTGAAGGCTGCGCTCAGAGGAACAAGCCAGGCGTGTACACA 2520

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RESULT 6
BC030532
LOCUS       BC030532               3273 bp    mRNA    linear   PRI 20-MAY-2002
DEFINITION  Homo sapiens, suppression of tumorigenicity 14 (colon carcinoma,
            matriptase, epithin), clone MGC:40392 IMAGE:5213189, mRNA, complete
            cds.
ACCESSION   BC030532
VERSION     BC030532.1  GI:20988874
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3273)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-MAY-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Laric,P., Legaspi,R., Maduro,Q.L.,
            Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C., McDowell,J.,
            Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C.,
            Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A.,
            Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
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            Series: IRAK Plate: 64 Row: k Column: 15
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Db        116 CCATGGGGAGCGATCGGGCCCGCAAGGGCGGAGGGGGCCCGAAGGACTTCGGCGCGGGAC 175

Qy        121 TCAAGTACAACTCCCGGCTAGAGAACATGAATGGCTTTGAGGAGGGTGTGGAGTTCCTGC 180

Db        176 TCAAGTACAACTCCCGGCACGAGAAAGTGAATGGCTTGGAGGAAGGCGTGGAGTTCCTGC 235

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RESULT 7
AF118224
LOCUS       AF118224                3149 bp    mRNA    linear   PRI 30-DEC-1999
DEFINITION  Homo sapiens matriptase mRNA, complete cds.
ACCESSION   AF118224
VERSION     AF118224.2  GI:6647301
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2955)
  AUTHORS   Lin,C.Y., Anders,J., Johnson,M., Sang,Q.A. and Dickson,R.B.
  TITLE     Molecular cloning of cDNA for matriptase, a matrix-degrading serine
            protease with trypsin-like activity
  JOURNAL   J. Biol. Chem. 274 (26), 18231-18236 (1999)
  MEDLINE   99303581
   PUBMED   10373424
REFERENCE   2  (bases 1 to 2955)
  AUTHORS   Lin,C.Y., Anders,J., Johnson,M., Sang,Q.A. and Dickson,R.B.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JAN-1999) Lombardi Cancer Center, Georgetown
            University Medical Center, 3970 Reservoir Road NW, Washington, DC
            20007, USA
REFERENCE   3  (bases 1 to 3149)
  AUTHORS   Oberst,M.D., Dickson,R.B. and Lin,C.Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-DEC-1999) Lombardi Cancer Center, Georgetown
            University Medical Center, 3970 Reservoir Road NW, Washington, DC
            20007, USA
  REMARK    Sequence update by submitter
COMMENT     On Dec 30, 1999 this sequence version replaced gi:5359674.
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ORIGIN

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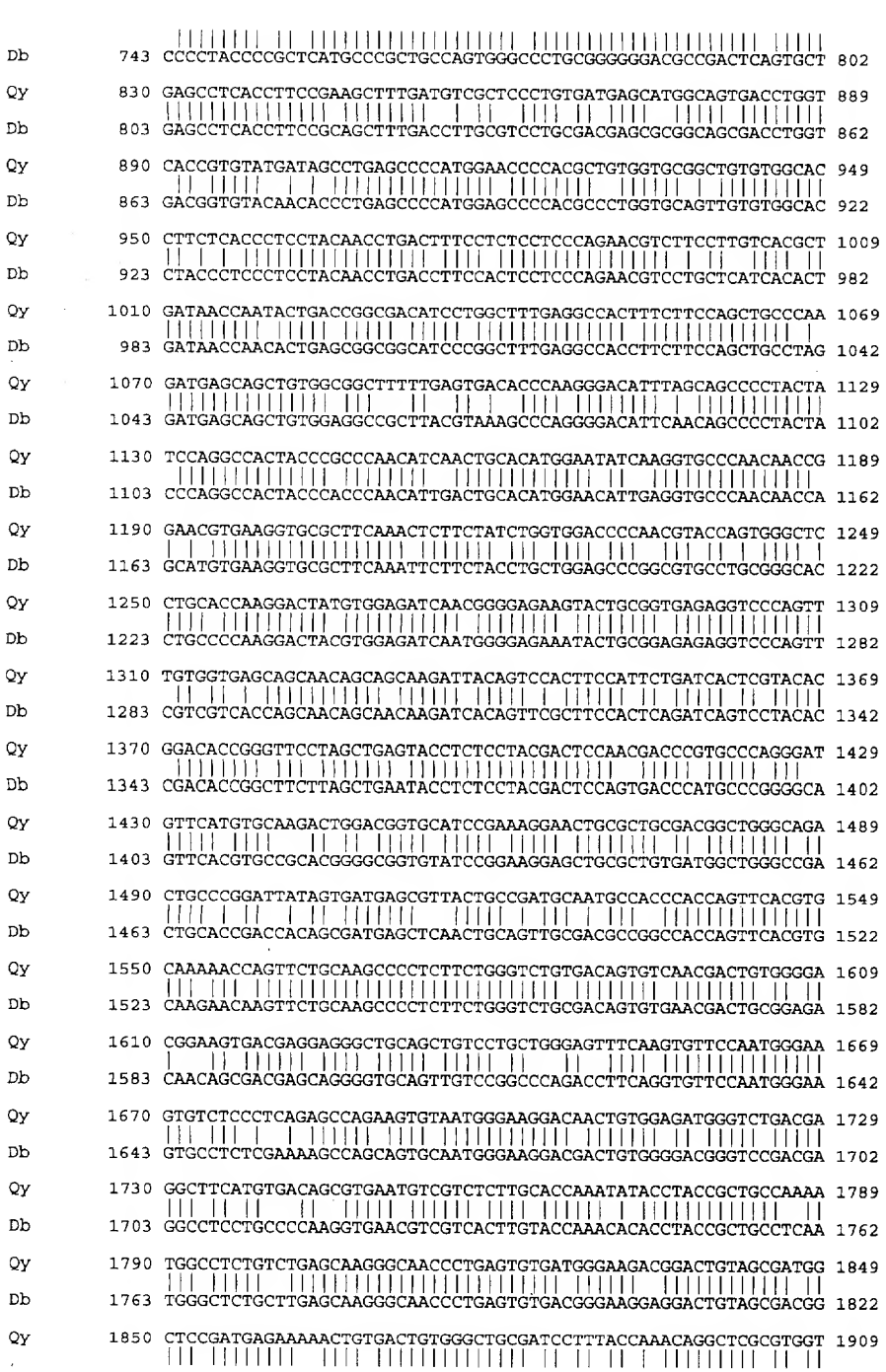

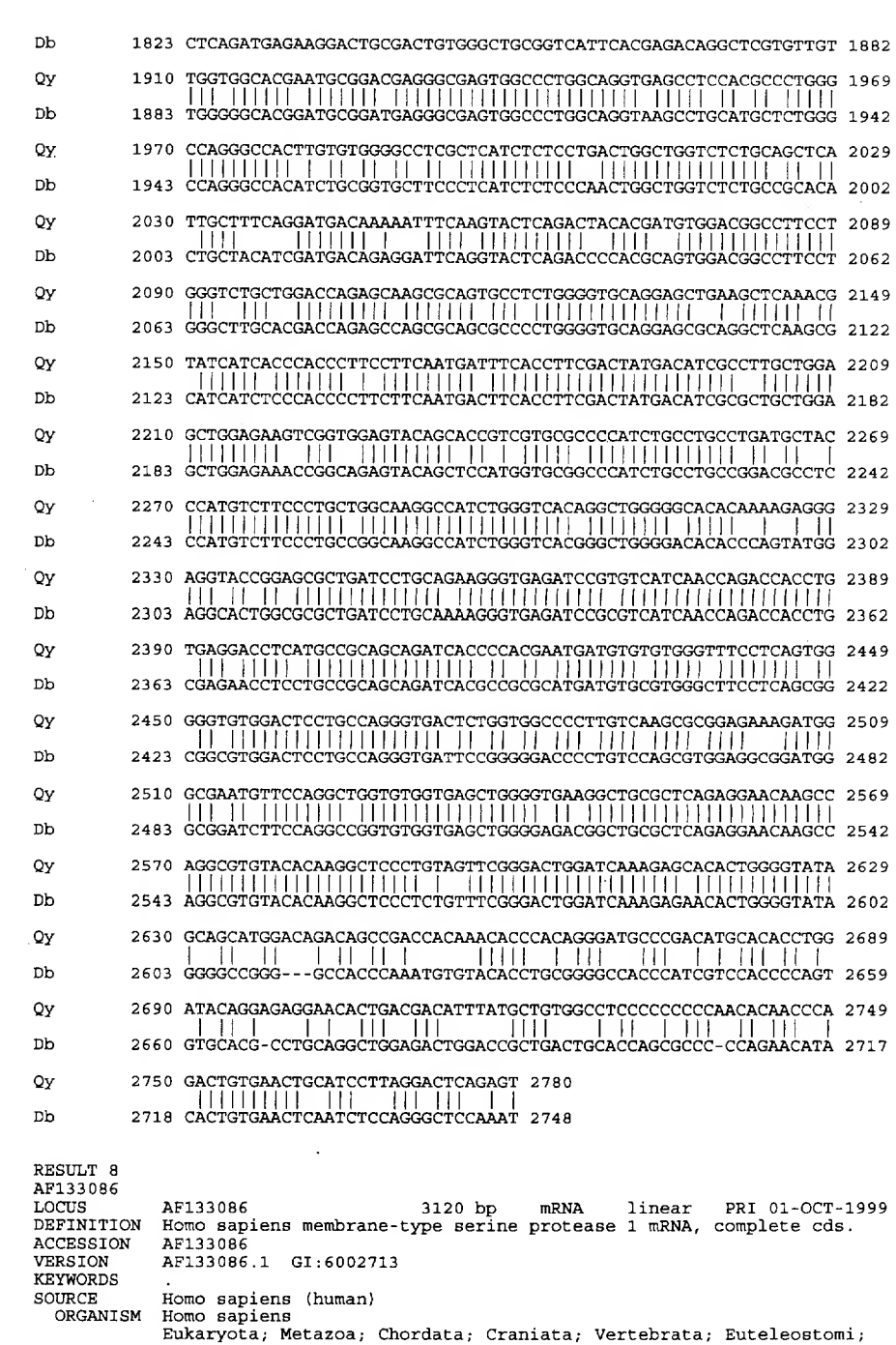

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DEFINITION Homo sapiens membrane-type serine protease 1 mRNA, complete cds.
ACCESSION AF133086
VERSION AF133086.1 GI:6002713
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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REFERENCE   1  (bases 1 to 3120)
  AUTHORS   Takeuchi,T., Shuman,M.A. and Craik,C.S.
  TITLE     Reverse biochemistry: use of macromolecular protease inhibitors to
            dissect complex biological processes and identify a membrane-type
            serine protease in epithelial cancer and normal tissue
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (20), 11054-11061 (1999)
  MEDLINE   99432178
   PUBMED   10500122
REFERENCE   2  (bases 1 to 3120)
  AUTHORS   Takeuchi,T., Shuman,M.A. and Craik,C.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-MAR-1999) Dept. Pharm. Chem., University of
            California, San Francisco, 513 Parnassus Ave., Box 0446, San
            Francisco, CA 94143-0446, USA
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ORIGIN

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  AUTHORS   Yamaguchi,N. and Mitsui,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-JUL-1999) Nozomi Yamaguchi, Kyoto Prefectural
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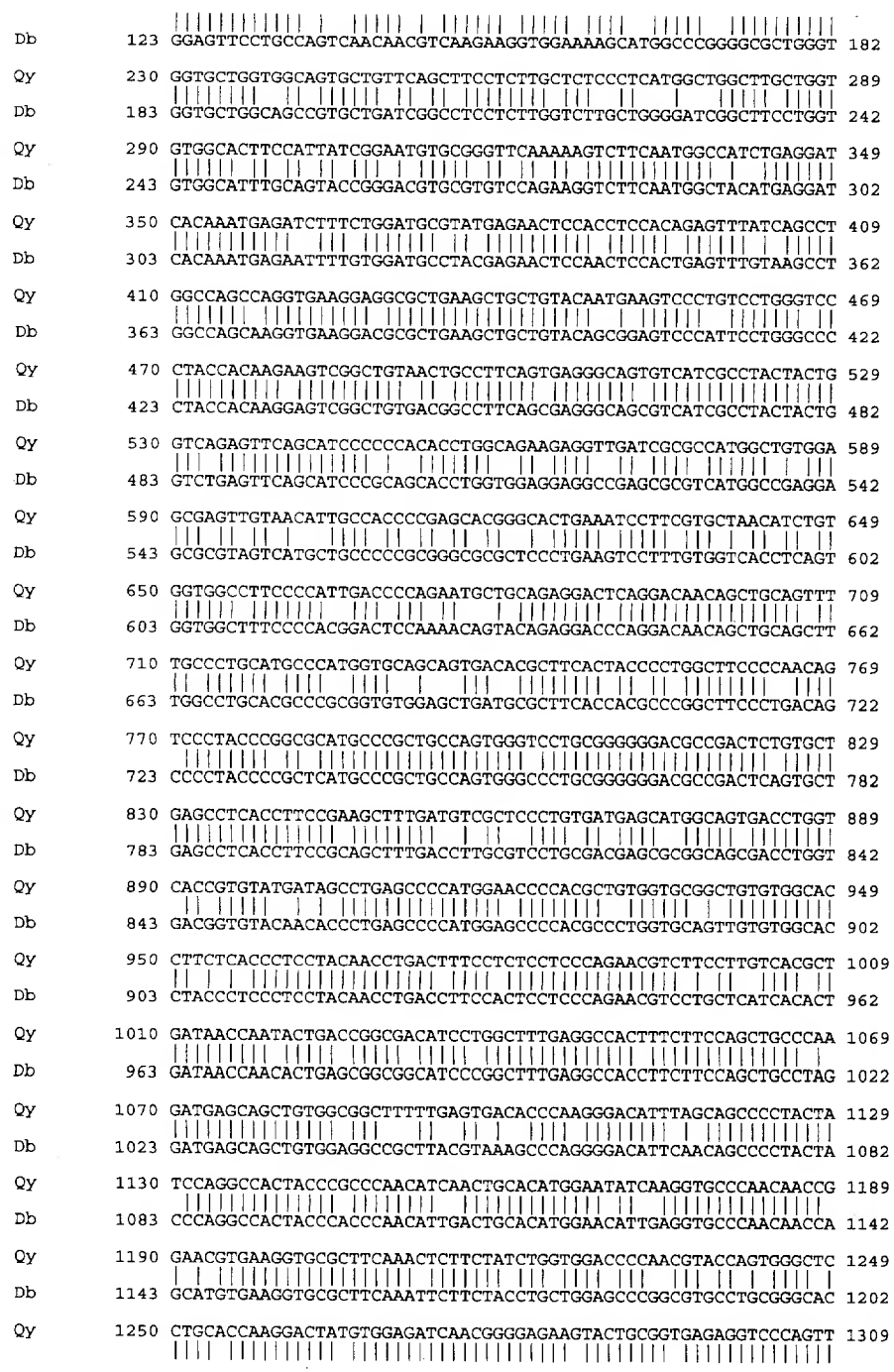
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  AUTHORS   O'Brien,T.J. and Tanimoto,H.
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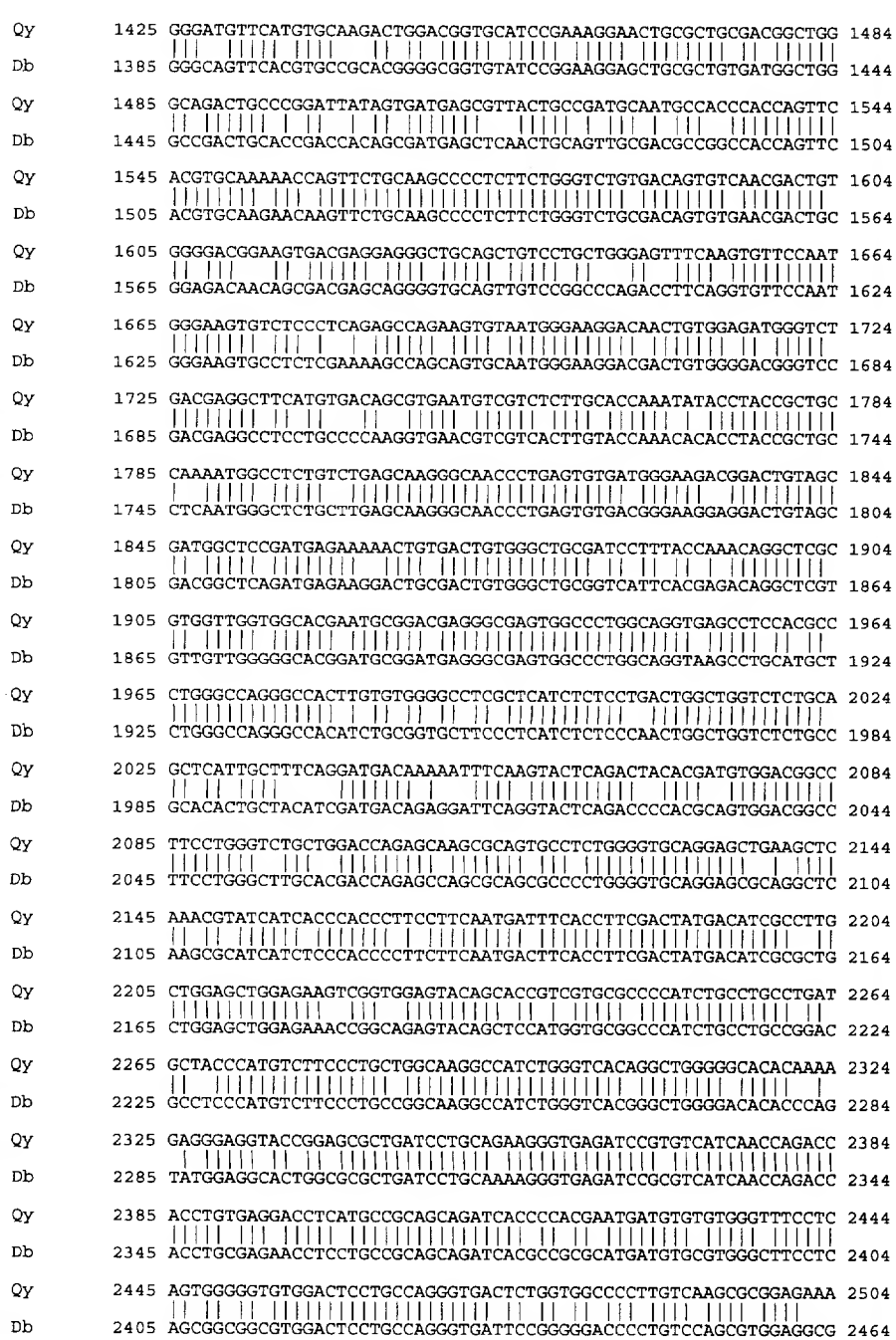

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REFERENCE 1 (bases 1 to 3147)
AUTHORS Leon,J.W.
TITLE Imaging member containing heat switchable carboxylate polymer and method of use
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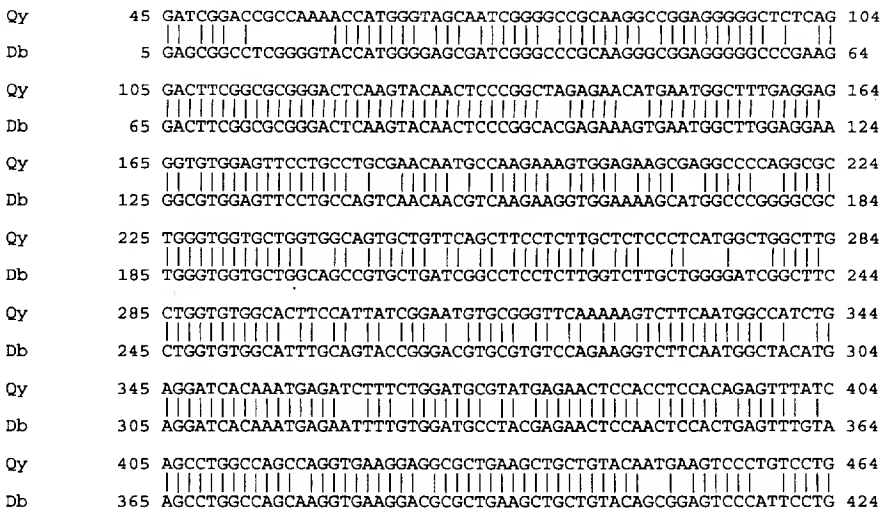

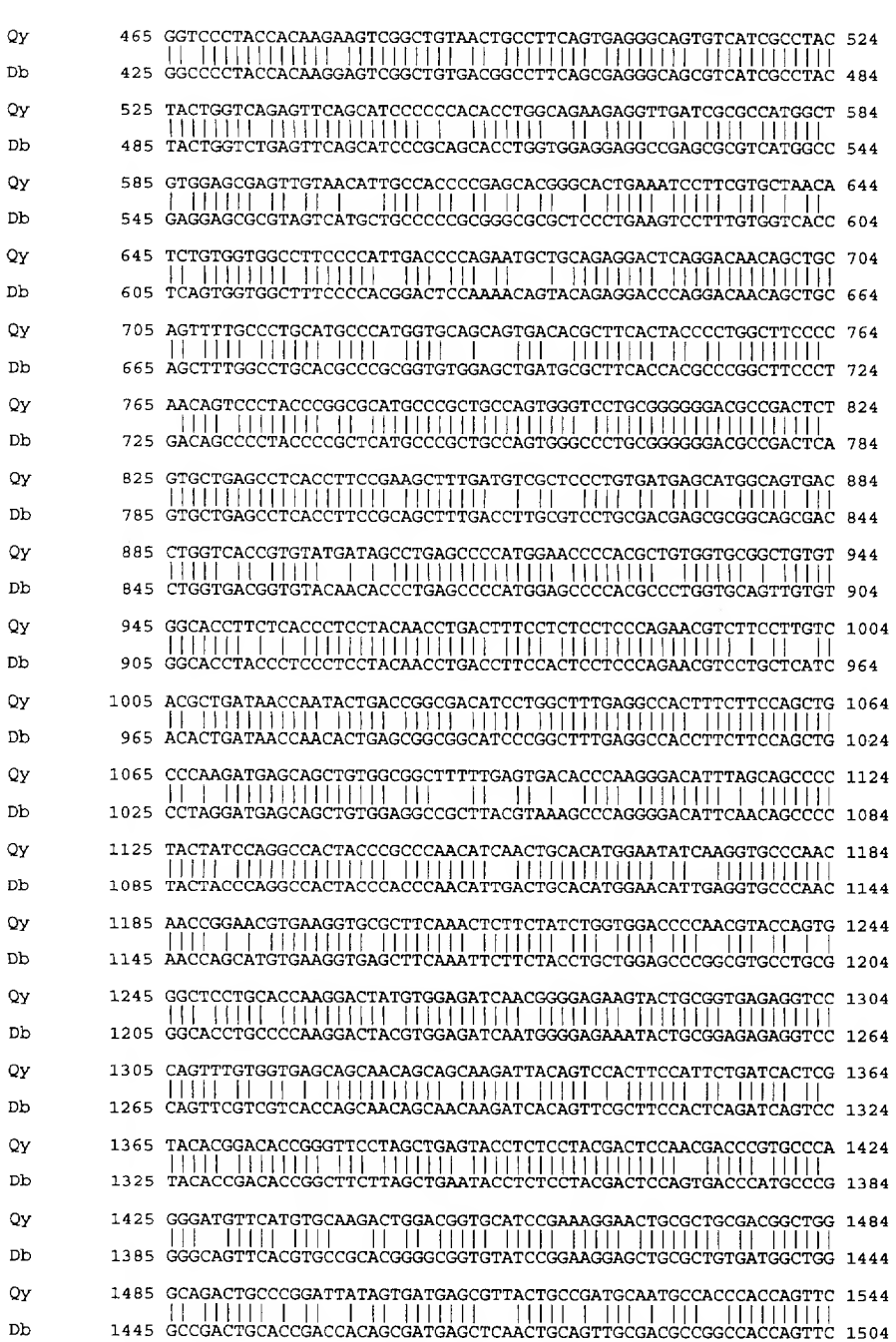

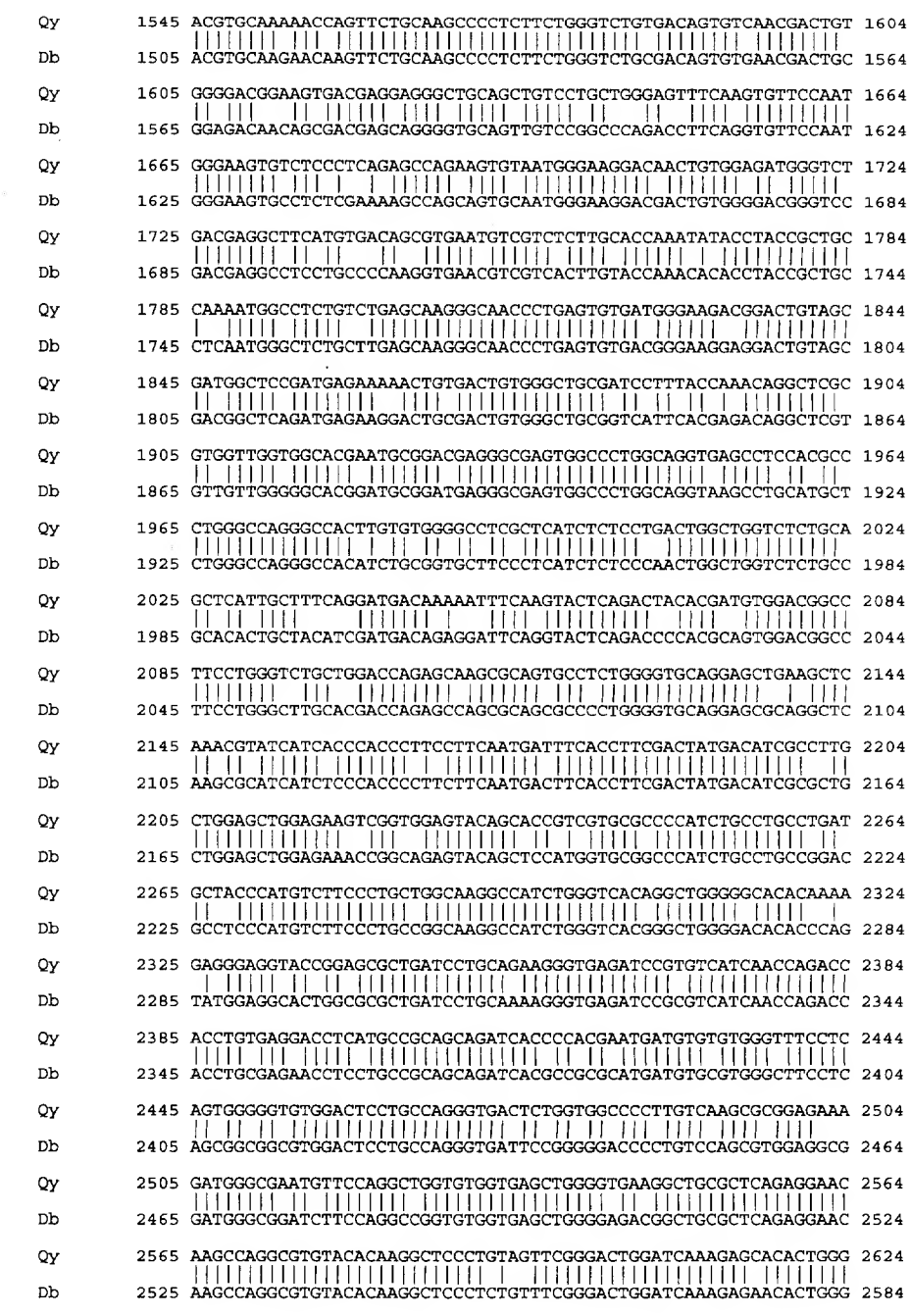

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Qy       2745 ACCCAGACTGTGAACTGCATCCTTAGGACTCAGAGT 2780

Db       2700 ACATACACTGTGAACTCAATCTCCAGGGCTCCAAAT 2735


RESULT 12
AR229712/c
LOCUS       AR229712                3147 bp    RNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 18 from patent US 6451500.
ACCESSION   AR229712
VERSION     AR229712.1  GI:27269442
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3147)
  AUTHORS   Leon,J.W.
  TITLE     Imaging member containing heat switchable carboxylate polymer and
            method of use
  JOURNAL   Patent: US 6451500-A 18 17-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .3147
                     /organism="unknown"
BASE COUNT      583 a    958 c    952 g    654 t
ORIGIN

  Query Match             60.6%;  Score 1883.2;  DB 6;  Length 3147;
  Best Local Similarity   81.2%;  Pred. No. 0;
  Matches 2223;  Conservative    0;  Mismatches  508;  Indels    5;  Gaps    3;

Qy         45 GATCGGACCGCCAAAACCATGGGTAGCAATCGGGGCCGCAAGGCCGGAGGGGGCTCTCAG 104

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Qy        285 CTGGTGTGGCACTTCCATTATCGGAATGTGCGGGTTCAAAAAGTCTTCAATGGCCATCTG 344

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Db       2723 GGCCCCTACCACAAGGAGTCGGCTGTGACGGCCTTCAGCGAGGGCAGCGTCATCGCCTAC 2664

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Db       2363 GTGCTGAGCCTCACCTTCCGCAGCTTTGACCTTGCGTCCTGCGACGAGCGCGGCAGCGAC 2304

Qy        885 CTGGTCACCGTGTATGATAGCCTGAGCCCCATGGAACCCCACGCTGTGGTGCGGCTGTGT 944

Db       2303 CTGGTGACGGTGTACAACACCCTGAGCCCCATGGAGCCCCACGCCCTGGTGCAGTTGTGT 2244

Qy        945 GGCACCTTCTCACCCTCCTACAACCTGACTTTCCTCTCCTCCCAGAACGTCTTCCTTGTC 1004

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Qy       1005 ACGCTGATAACCAATACTGACCGGCGACATCCTGGCTTTGAGGCCACTTTCTTCCAGCTG 1064

Db       2183 ACACTGATAACCAACACTGAGCGGCGGCATCCCGGCTTTGAGGCCACCTTCTTCCAGCTG 2124

Qy       1065 CCCAAGATGAGCAGCTGTGGCGGCTTTTTGAGTGACACCCAAGGGACATTTAGCAGCCCC 1124

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Db       1763 GGGCAGTTCACGTGCCGCACGGGGCGGTGTATCCGGAAGGAGCTGCGCTGTGATGGCTGG 1704

Qy       1485 GCAGACTGCCCGGATTATAGTGATGAGCGTTACTGCCGATGCAATGCCACCCACCAGTTC 1544

Db       1703 GCCGACTGCACCGACCACAGCGATGAGCTCAACTGCAGTTGCGACGCCGGCCACCAGTTC 1644

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Qy       1665 GGGAAGTGTCTCCCTCAGAGCCAGAAGTGTAATGGGAAGGACAACTGTGGAGATGGGTCT 1724
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Qy      1845 GATGGCTCCGATGAGAAAAACTGTGACTGTGGGCTGCGATCCTTTACCAAACAGGCTCGC 1904

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Db       983 CTGGAGCTGGAGAAACCGGCAGAGTACAGCTCCATGGTGCGGCCCATCTGCCTGCCGGAC 924

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Qy      2565 AAGCCAGGCGTGTACACAAGGCTCCCTGTAGTTCGGGACTGGATCAAAGAGCACACTGGG 2624

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Qy      2625 GTATAGCAGCATGGACAGACAGCCGACCACAAACACCCACAGGGATGCCCGACATGCACA 2684

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Db       506 CCAGTGTGCACG-CCTGCAGGCTGGAGACTGGACCGCTGACTGCACCAGCGCCC-CCAGA 449

Qy      2745 ACCCAGACTGTGAACTGCATCCTTAGGACTCAGAGT 2780
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DEFINITION  Sequence 1 from Patent WO0157194.
ACCESSION   AX207897
VERSION     AX207897.1  GI:15422495
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Madison,E.L., Ong,E.O. and Yeh,J.C.
  TITLE     Nucleic acid molecules encoding transmembrane serine proteases, the
            encoded proteins and methods based thereon
  JOURNAL   Patent: WO 0157194-A 1 09-AUG-2001;
            CORVAS INTERNATIONAL, INC. (US)
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BASE COUNT      654 a    952 c    958 g    583 t
ORIGIN
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  Query Match           60.6%;  Score 1883.2;  DB 6;  Length 3147;
  Best Local Similarity   81.2%;  Pred. No. 0;
  Matches 2223;  Conservative    0;  Mismatches  508;  Indels    5;  Gaps    3;

Qy         45 GATCGGACCGCCAAAACCATGGGTAGCAATCGGGGCCGCAAGGCCGGAGGGGGCTCTCAG 104

Db          5 GAGCGGCCTCGGGGTACCATGGGGAGCGATCGGGCCCGCAAGGGCGGAGGGGGCCCGAAG 64

Qy        105 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCTAGAGAACATGAATGGCTTTGAGGAG 164

Db         65 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCACGAGAAAGTGAATGGCTTGGAGGAA 124

Qy        165 GGTGTGGAGTTCCTGCCTGCGAACAATGCCAAGAAAGTGGAGAAGCGAGGCCCCAGGCGC 224

Db        125 GGCGTGGAGTTCCTGCCAGTCAACAACGTCAAGAAGGTGGAAAAGCATGGCCCGGGGCGC 184

Qy        225 TGGGTGGTGCTGGTGGCAGTGCTGTTCAGCTTCCTCTTGCTCTCCCTCATGGCTGGCTTG 284

Db        185 TGGGTGGTGCTGGCAGCCGTGCTGATCGGCCTCCTCTTGGTCTTGCTGGGGATCGGCTTC 244

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Qy       2685 CCTGGATACAGGAGAGGAACACTGACGACATTTATGCTGTGGCCTCCCCCCCCCAACACA 2744
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Db       2642 CCAGTGTGCACG-CCTGCAGGCTGGAGACTGGACCGCTGACTGCACCAGCGCCC-CCAGA 2699

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RESULT 14
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DEFINITION  Sequence 49 from Patent WO0157194.
ACCESSION   AX207945
VERSION     AX207945.1  GI:15422543
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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REFERENCE   1
  AUTHORS   Madison,E.L., Ong,E.O. and Yeh,J.C.
  TITLE     Nucleic acid molecules encoding transmembrane serine proteases, the
            encoded proteins and methods based thereon
  JOURNAL   Patent: WO 0157194-A 49 09-AUG-2001;
            CORVAS INTERNATIONAL, INC. (US)
FEATURES             Location/Qualifiers
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BASE COUNT      654 a    952 c    958 g    583 t
ORIGIN

  Query Match             60.6%;  Score 1883.2;  DB 6;  Length 3147;
  Best Local Similarity   81.2%;  Pred. No. 0;
  Matches 2223;  Conservative    0;  Mismatches  508;  Indels    5;  Gaps    3;

Qy         45 GATCGGACCGCCAAAACCATGGGTAGCAATCGGGGCCGCAAGGCCGGAGGGGGCTCTCAG 104
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Qy        105 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCTAGAGAACATGAATGGCTTTGAGGAG 164
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Qy        165 GGTGTGGAGTTCCTGCCTGCGAACAATGCCAAGAAAGTGGAGAAGCGAGGCCCCAGGCGC 224
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Db        125 GGCGTGGAGTTCCTGCCAGTCAACAACGTCAAGAAGGTGGAAAAGCATGGCCCGGGGCGC 184

Qy        225 TGGGTGGTGCTGGTGGCAGTGCTGTTCAGCTTCCTCTTGCTCTCCCTCATGGCTGGCTTG 284
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Qy        465 GGTCCCTACCACAAGAAGTCGGCTGTAACTGCCTTCAGTGAGGGCAGTGTCATCGCCTAC 524
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DEFINITION  Homo sapiens serine protease TADG15 mRNA, complete cds.
ACCESSION   AF057145
VERSION     AF057145.1  GI:10257389
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3147)
  AUTHORS   Tanimoto,H., Underwood,L.J., Wang,Y., Shigemasa,K., Parmley,T.H.
            and O'Brien,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-APR-1998) Biochemistry, University of Arkansas for
            Medical Sciences, 4301 W. Markham St., Little Rock, AR 72205, USA
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BASE COUNT      654 a    952 c    958 g    583 t
ORIGIN
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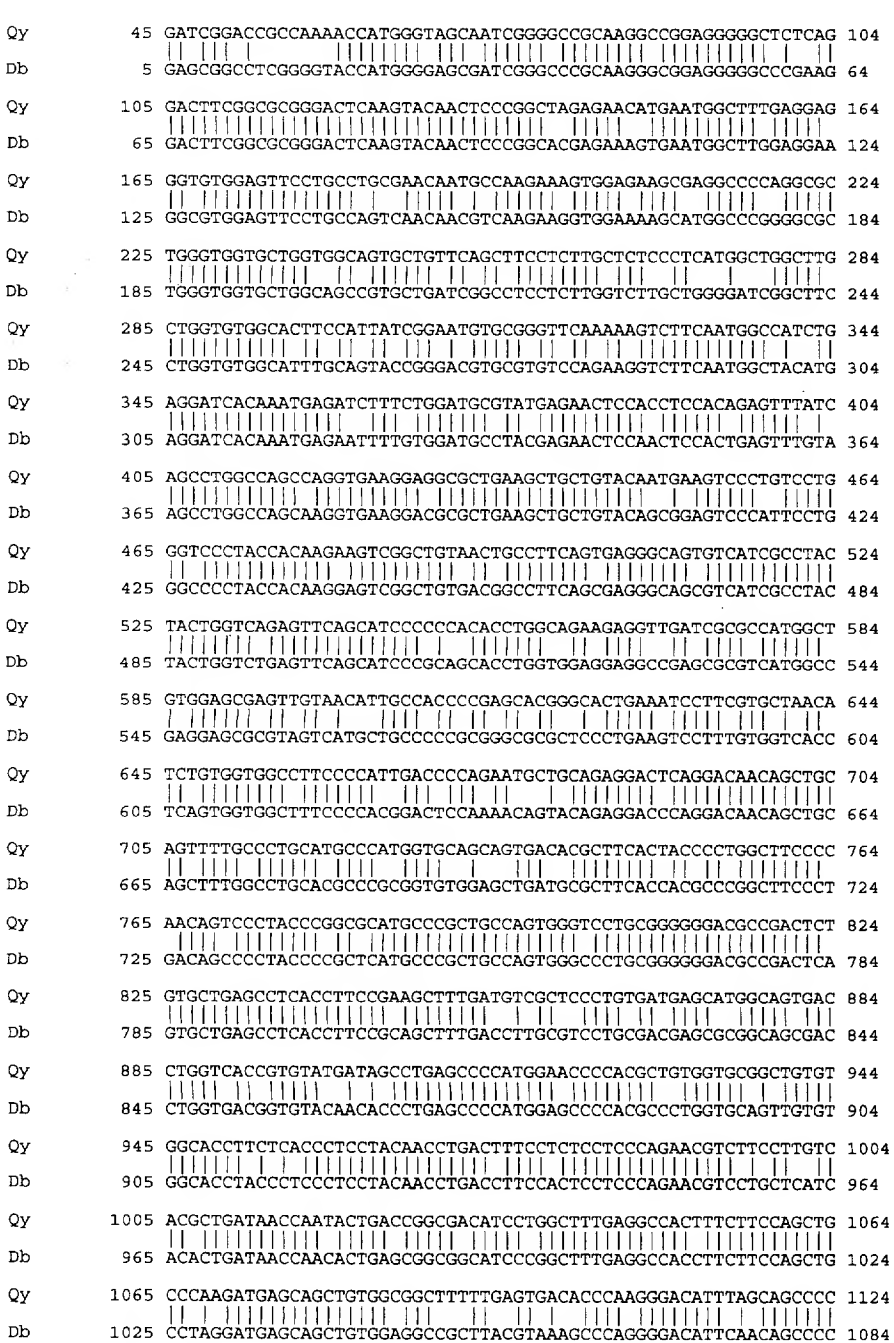

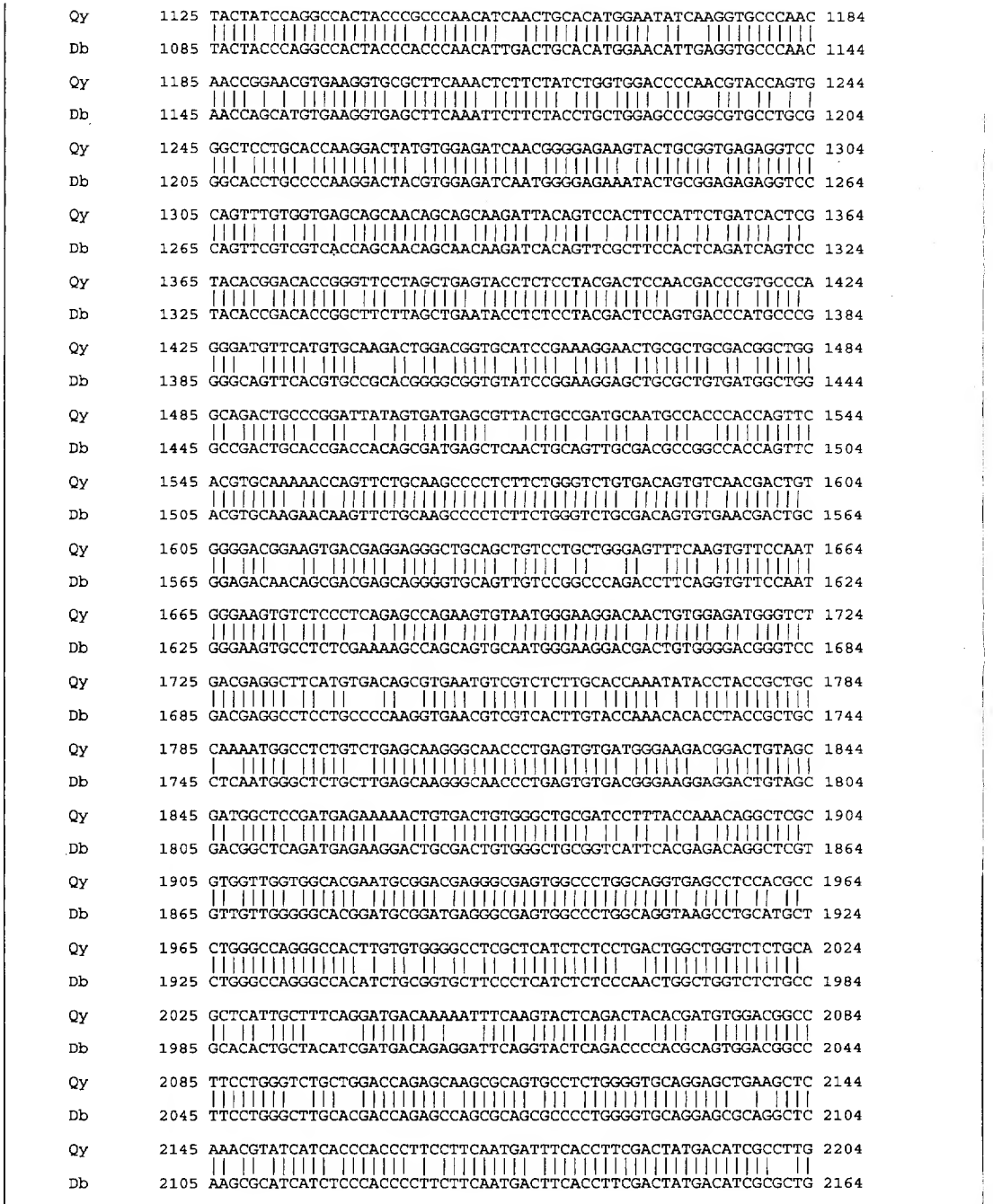

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Qy       2325 GAGGGAGGTACCGGAGCGCTGATCCTGCAGAAGGGTGAGATCCGTGTCATCAACCAGACC 2384

Db       2285 TATGGAGGCACTGGCGCGCTGATCCTGCAAAAGGGTGAGATCCGCGTCATCAACCAGACC 2344

Qy       2385 ACCTGTGAGGACCTCATGCCGCAGCAGATCACCCCACGAATGATGTGTGTGGGTTTCCTC 2444

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Qy       2625 GTATAGCAGCATGGACAGACAGCCGACCACAAACACCCACAGGGATGCCCGACATGCACA 2684

Db       2585 GTATAGGGGCCGGG---GCCACCCAAATGTGTACACCTGCGGGGCCACCCATCGTCCACC 2641

Qy       2685 CCTGGATACAGGAGAGGAACACTGACGACATTTATGCTGTGGCCTCCCCCCCCCAACACA 2744

Db       2642 CCAGTGTGCACG-CCTGCAGGCTGGAGACTGGACCGCTGACTGCACCAGCGCCC-CCAGA 2699

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Job time : 11176 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 21, 2004, 02:03:32 ; Search time 795 Seconds
(without alignments)
10546.484 Million cell updates/sec

Title: US-09-900-751-1
Perfect score: 3106
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	5	1883.2	60.6	3147	22	AAD13113	Human membrane-typ
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	7	1883.2	60.6	3147	22	AAH23601	Human TADG-15 codi
c	8	1883.2	60.6	3147	22	AAH23609	Human TADG-15 anti
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	11	1883.2	60.6	3147	25	ABZ58500	Transmembrane seri
	12	1883.2	60.6	3147	25	ABZ58501	Transmembrane seri
	13	1883.2	60.6	3147	25	ABZ22450	Human membrane-typ
	14	1883.2	60.6	3147	25	ABZ22451	Human MTSP1 protea
	15	1883.2	60.6	3147	25	AAD47180	Human membrane-typ
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	22	1762.2	56.7	2955	21	AAA88492	Human matriptase (
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	24	1532.4	49.3	3112	24	ABS76526	cDNA encoding huma
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	26	1530.8	49.3	2900	24	ABK84260	Human cDNA differe
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	35	306.8	9.9	434	25	ACA02957	Lung cancer therap
	36	302.6	9.7	429	24	ABL82332	Human ovarian canc
	37	279.2	9.0	387	23	AAS85626	DNA encoding novel
	38	265	8.5	591	23	AAS58827	cDNA #1503 encodin
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ALIGNMENTS

RESULT 1
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ID AAD37039 standard; DNA; 3106 BP.
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AC AAD37039;
XX
DT 21-AUG-2002 (first entry)
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DE Epithin gene.
XX
KW Transgenic; transgenic animal; pharmacological therapy; gene therapy;
KW phenotype modulation; genetic disease; epithin; gene; ds.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
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PD 17-JAN-2002.
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PF 06-JUL-2001; 2001WO-US21427.
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PR 06-JUL-2000; 2000US-216109P.
PR 06-JUL-2000; 2000US-216251P.
PR 06-JUL-2000; 2000US-216258P.
PR 06-JUL-2000; 2000US-216768P.
PR 10-JUL-2000; 2000US-217449P.
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PR 26-OCT-2000; 2000US-244037P.
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PR 26-JUN-2001; 2001US-301217P.
XX
PA (DELT-) DELTAGEN INC.
XX
PI Allen KD, Leviten MW;
XX
DR WPI; 2002-154853/20.
DR P-PSDB; AAE23083.
XX
PT Novel non-human transgenic animal, preferably transgenic mice
PT comprising disruption in target gene, e.g., tryptase gene, useful for
PT identifying an agent that modulates expression or function of target
PT gene -
XX
PS Example 2; Fig 2A; 74pp; English.
XX
CC The present invention relates to non-human transgenic animals preferably
CC transgenic mice comprising disruption in target gene such as tryptase
CC gene. The invention also relates to compositions and methods relating
CC to the characterisation of gene functions. The transgenic animals are
CC useful for identifying an agent that modulates the expression or function
CC of a target. They are useful for identifying an agent that modulates a
CC phenotype associated with a disruption in tryptase genes or limulus
CC clotting factor protease-like genes by administering an agent to the
CC transgenic animal and determining whether the agent modulates the
CC phenotype where the agent has effect on decreased body weight, decreased
CC thymus weight, decreased thymus to body weight ratio, increased pre-pulse
CC inhibition, significant decrease in their response latency to the hot
CC plate test or a decreased response threshold to metrazol. Agents that
CC modulate the expression, function or activity of the target gene are
CC useful for treating a disorder associated with a mutation in tryptase
CC gene or in limulus clotting factor protease-like gene. The transgenic
CC animals are useful for testing the efficacy of proposed genetic and
CC pharmacological therapies for human genetic diseases. They are useful
CC as models for diseases, disorders or conditions associated with
CC phenotypes relating to a disruption in a target and to identify drugs,
CC pharmaceuticals, therapies and interventions which may be effective in
CC treating a disease or other phenotypic characteristics of the animal.
CC The present sequence is epithin gene. This sequence is used in the
CC exemplification of the invention.
XX
SQ Sequence 3106 BP; 692 A; 862 C; 897 G; 655 T; 0 other;

Query Match 100.0%; Score 3106; DB 24; Length 3106;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        121 TCAAGTACAACTCCCGGCTAGAGAACATGAATGGCTTTGAGGAGGGTGTGGAGTTCCTGC 180
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Qy        181 CTGCGAACAATGCCAAGAAAGTGGAGAAGCGAGGCCCCAGGCGCTGGGTGGTGCTGGTGG 240
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Db        181 CTGCGAACAATGCCAAGAAAGTGGAGAAGCGAGGCCCCAGGCGCTGGGTGGTGCTGGTGG 240

Qy        241 CAGTGCTGTTCAGCTTCCTCTTGCTCTCCCTCATGGCTGGCTTGCTGGTGTGGCACTTCC 300
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Db        241 CAGTGCTGTTCAGCTTCCTCTTGCTCTCCCTCATGGCTGGCTTGCTGGTGTGGCACTTCC 300

Qy        301 ATTATCGGAATGTGCGGGTTCAAAAAGTCTTCAATGGCCATCTGAGGATCACAAATGAGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        361 TCTTTCTGGATGCGTATGAGAACTCCACCTCCACAGAGTTTATCAGCCTGGCCAGCCAGG 420
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Qy        481 AGTCGGCTGTAACTGCCTTCAGTGAGGGCAGTGTCATCGCCTACTACTGGTCAGAGTTCA 540
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Qy        541 GCATCCCCCCACACCTGGCAGAAGAGGTTGATCGCGCCATGGCTGTGGAGCGAGTTGTAA 600
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Qy        781 CGCATGCCCGCTGCCAGTGGGTCCTGCGGGGGGACGCCGACTCTGTGCTGAGCCTCACCT 840
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Qy        901 ATAGCCTGAGCCCCATGGAACCCCACGCTGTGGTGCGGCTGTGTGGCACCTTCTCACCCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATAGCCTGAGCCCCATGGAACCCCACGCTGTGGTGCGGCTGTGTGGCACCTTCTCACCCT 960

Qy        961 CCTACAACCTGACTTTCCTCTCCTCCCAGAACGTCTTCCTTGTCACGCTGATAACCAATA 1020
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Qy       3061 TTGAGAGTAAAACATTTTATTTCTTTTTAAAAAAAAAAAAAAAAAA 3106
Db       3061 TTGAGAGTAAAACATTTTATTTCTTTTTAAAAAAAAAAAAAAAAAA 3106
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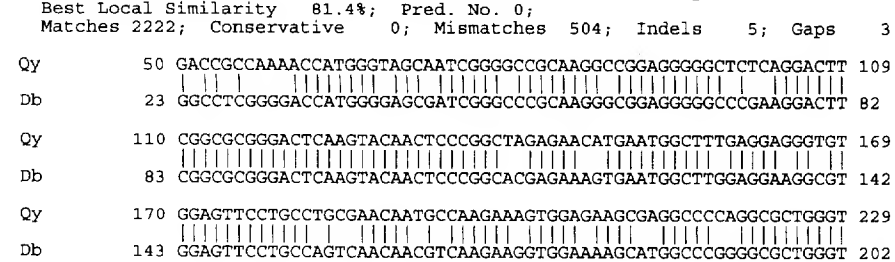
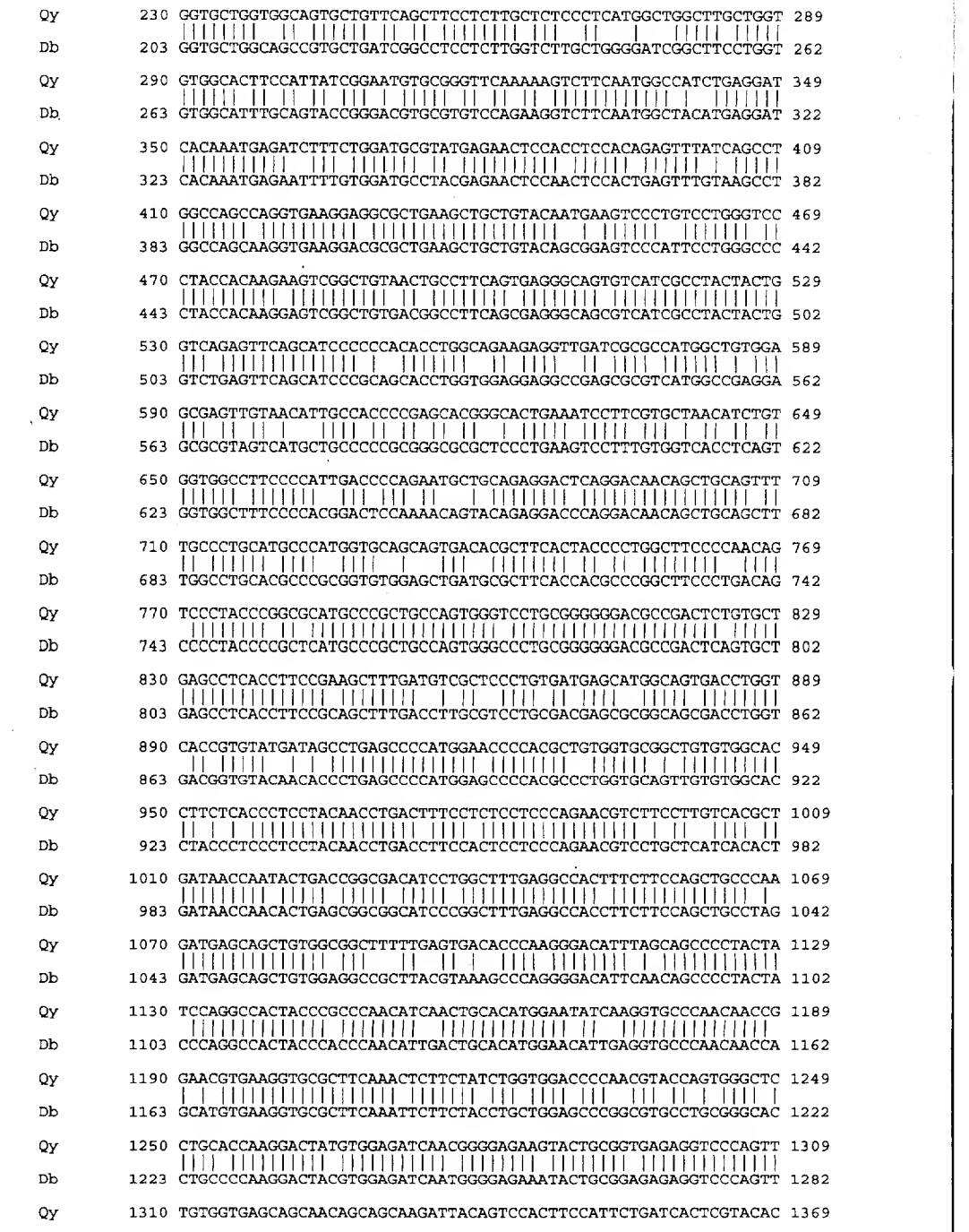
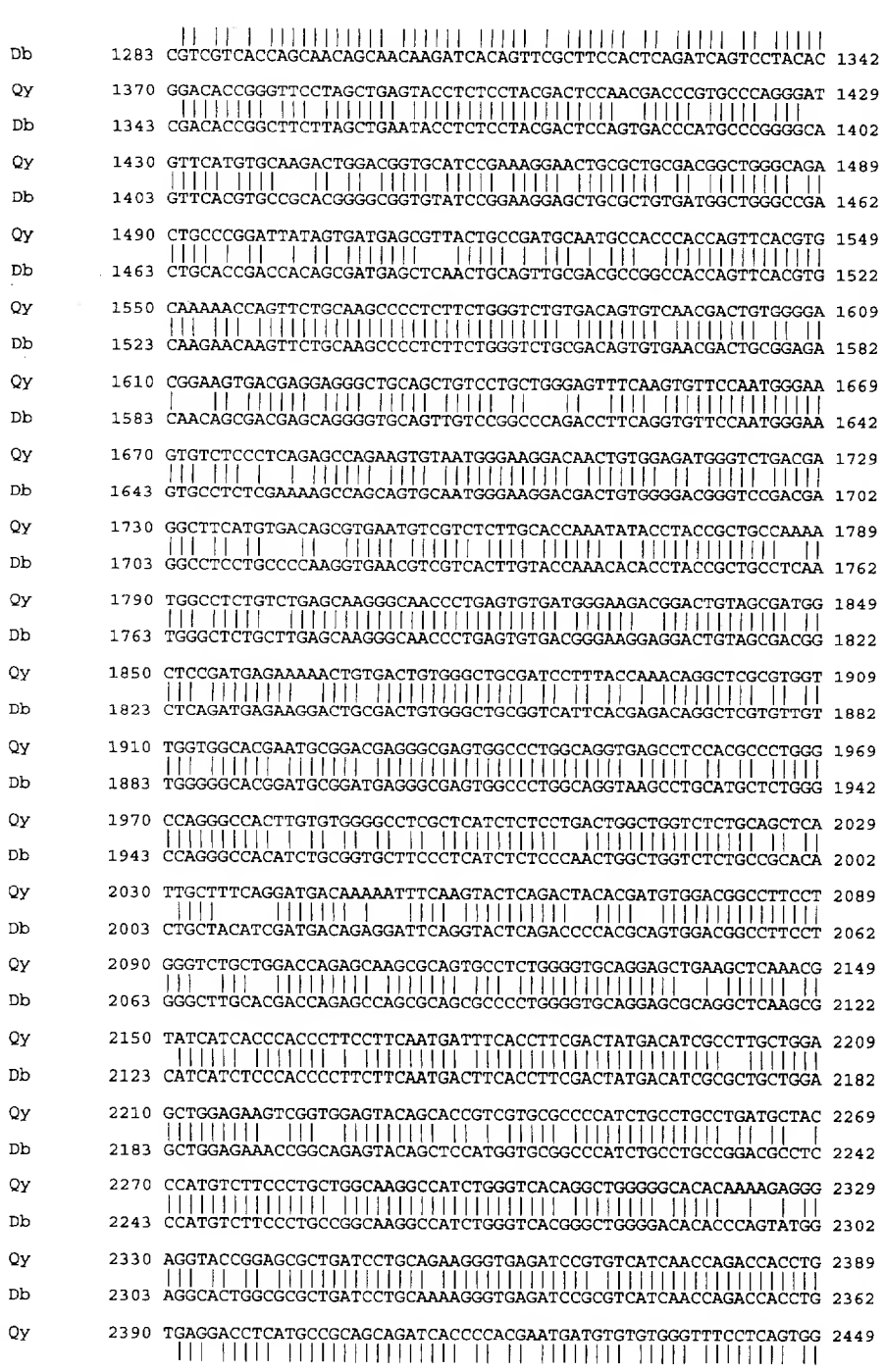
RESULT 2
AAA88493
ID   AAA88493 standard; cDNA; 3149 BP.
XX
AC   AAA88493;
XX
DT   22-JAN-2001  (first entry)
XX
DE   Human matriptase cDNA.
XX
KW   Matriptase; serine protease; human; breast cancer; pre-malignancy;
KW   actinic keratosis; leukoplakia; Barrett's epithelium;
KW   columnar metaplasia; ulcerative colitis; bowenoid papulosis;
KW   adenomatous colorectal polyp; Qyerat erythroplasia;
KW   vulvar intraepithelial neoplasia; tumour; metastasis; therapy; ss.
```

XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 36..2603
FT /*tag= c
XX
PN WO200053232-A1.
XX
PD 14-SEP-2000.
XX
PF 10-MAR-2000; 2000WO-US06111.
XX
PR 12-MAR-1999; 99US-0124006.
XX
PA (GEOU) UNIV GEORGETOWN.
XX
PI Dickson RB, Lin C, Johnson M, Wang S, Enyedy I;
XX
DR WPI; 2000-594268/56.
DR P-PSDB; AAB19552.
XX
PT Treating malignancies, premalignant and pathologic conditions in a
PT subject, comprises administering matriptase modulating agent -
XX
PS Claim 9; Fig 15; 116pp; English.
XX
CC The present sequence is that of cDNA coding for the full-length
CC form (see AAB19521) of human matriptase, a trypsin-like protease.
CC cDNA encoding a truncated form of matriptase is given in AAA88492.
CC Either form can be incorporated into a vector and used in a claimed
CC method for making recombinant matriptase. The zymogen (inactive)
CC form of matriptase is a single-chain protein. The active 2-chain
CC form strongly interacts with fragments of a Kunitz-type serine
CC protease inhibitor (hepatocyte growth factor activator inhibitor,
CC HAI-1) to form SDS-stable complexes. In breast cancer cells,
CC matriptase is present mainly as the uncomplexed form. Only the
CC complexed matriptase in detected in human milk. The invention is
CC directed to a method of detecting a malignancy or a pre-malignant
CC lesion in breast or other tissue by detecting the presence of
CC single- or 2-chain forms of matriptase in the tissue. The
CC object is to inhibit tumour onset, tumour growth and metastasis.
CC Malignancies and pre-malignant conditions characterised by
CC expression of the zymogen or activated form of matriptase are
CC treated by administering an inhibitor of matriptase, especially a
CC Bowman-Birk inhibitor. The pre-malignant condition is atypical
CC ductal hyperplasia of the breast, actinic keratosis, leukoplakia,
CC Barrett's epithelium of the esophagus, ulcerative colitis,
CC adenomatous colorectal polyps, erythroplasia of the Queyrat,
CC Bowen's disease, bowenoid papulosis, vulvar intraepithelial
CC neoplasia or dysplatic changes to the cervix. The invention also
CC provides methods for in vivo or in vitro diagnosis of malignancy
CC or pre-malignant lesion, and methods of identifying matriptase
CC modulators, including activators and inhibitors.
XX
SQ Sequence 3149 BP; 647 A; 959 C; 962 G; 581 T; 0 other;

Query Match 60.8%; Score 1889.8; DB 21; Length 3149;
Best Local Similarity 81.4%; Pred. No. 0;
Matches 2222; Conservative 0; Mismatches 504; Indels 5; Gaps 3;



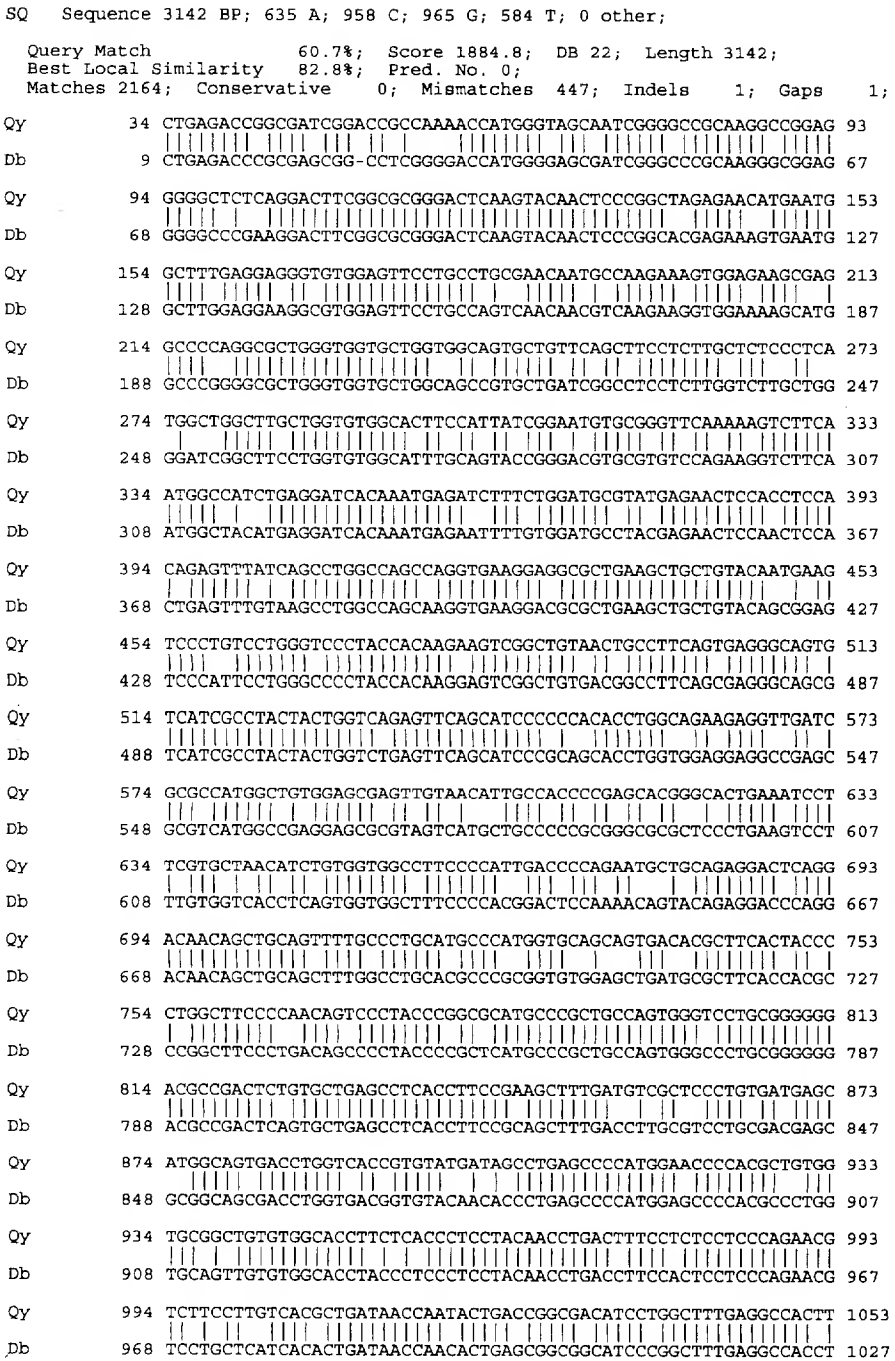


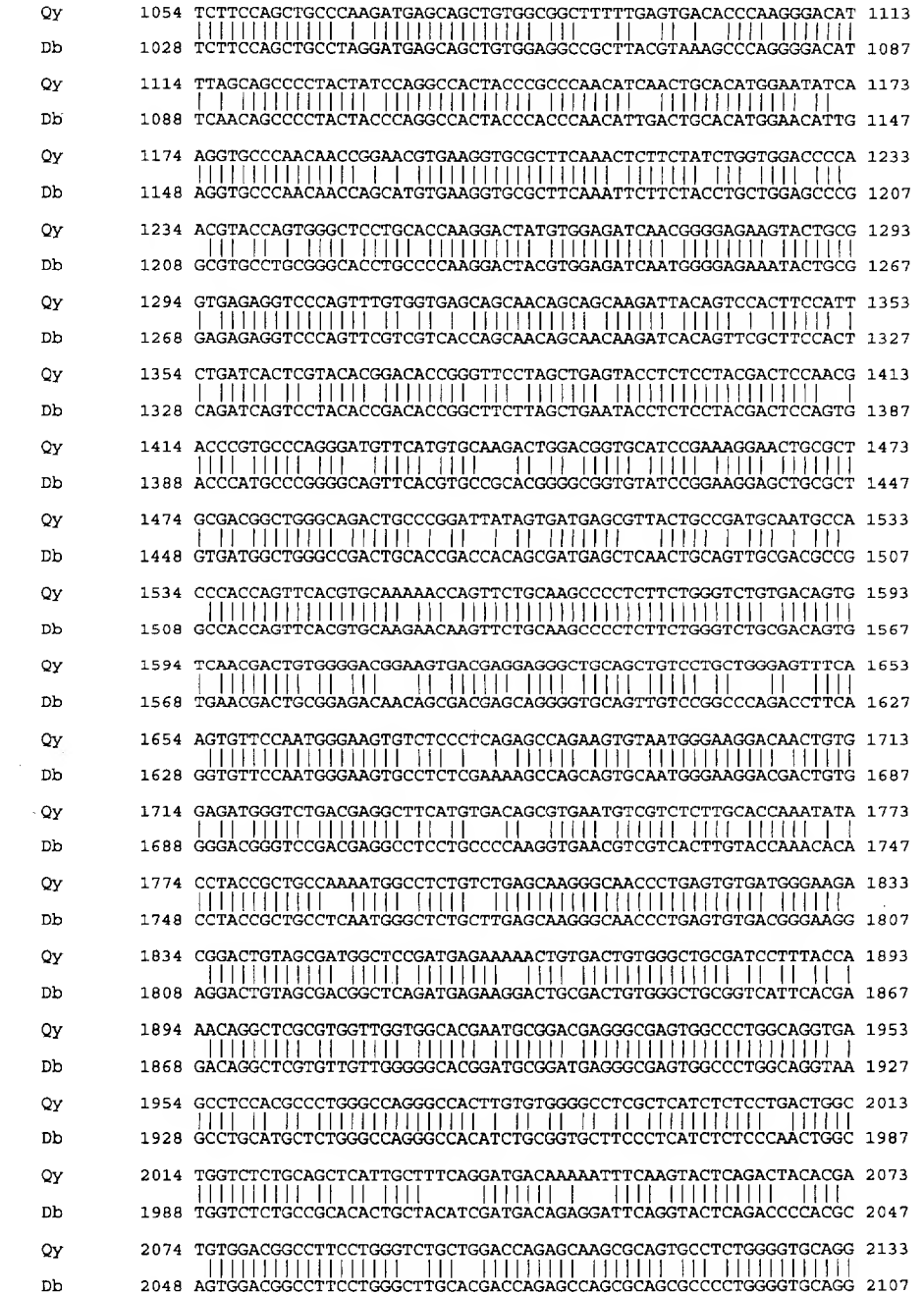


RESULT 3
AAF28099
ID AAF28099 standard; cDNA; 3142 BP.
XX
AC AAF28099;
XX
DT 06-JUN-2001 (first entry)
XX
DE Human membrane-type serine protease MT-SP1 coding sequence.
XX
KW Human; membrane-type serine protease; MT-SP1; cancer; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 37..2602
FT /*tag= a
FT /product= "MT-SP1"
XX
PN WO200123524-A2.
XX
PD 05-APR-2001.
XX
PF 02-OCT-2000; 2000WO-US27250.
XX
PR 30-SEP-1999; 99US-0410362.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Craik CS, Takeuchi T, Shuman M;
XX
DR WPI; 2001-245002/25.
DR P-PSDB; AAB35465.
XX
PT New nucleic acid encoding a membrane type serine protease, useful for
PT the diagnosis, prognosis and treatment of cancer, particularly
PT metastatic cancers -
XX
PS Claim 4; Fig 1; 102pp; English.
XX
CC The present invention provides the protein and coding sequences for the
CC novel human membrane-type serine protease MT-SP1. Increased expression of
CC this protein is associated with cancer, and so the sequences can be used
CC in cancer diagnosis and the identification of treatments. The present
CC sequence is the MT-SP1 coding sequence.
XX

SQ Sequence 3142 BP; 635 A; 958 C; 965 G; 584 T; 0 other;

Query Match 60.7%; Score 1884.8; DB 22; Length 3142;
Best Local Similarity 82.8%; Pred. No. 0;
Matches 2164; Conservative 0; Mismatches 447; Indels 1; Gaps 1;





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Qy       2134 AGCTGAAGCTCAAACGTATCATCACCCACCCTTCCTTCAATGATTTCACCTTCGACTATG 2193
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Qy       2194 ACATCGCCTTGCTGGAGCTGGAGAAGTCGGTGGAGTACAGCACCGTCGTGCGCCCCATCT 2253
Db       2168 ACATCGCGCTGCTGGAGCTGGAGAAACCGGCAGAGTACAGCTCCATGGTGCGGCCCATCT 2227

Qy       2254 GCCTGCCTGATGCTACCCATGTCTTCCCTGCTGGCAAGGCCATCTGGGTCACAGGCTGGG 2313
Db       2228 GCCTGCCGGACGCCTCCCATGTCTTCCCTGCCGGCAAGGCCATCTGGGTCACGGGCTGGG 2287

Qy       2314 GGCACACAAAAGAGGGAGGTACCGGAGCGCTGATCCTGCAGAAGGGTGAGATCCGTGTCA 2373
Db       2288 GACACACCCAGTATGGAGGCACTGGCGCGCTGATCCTGCAAAAGGGTGAGATCCGCGTCA 2347

Qy       2374 TCAACCAGACCACCTGTGAGGACCTCATGCCGCAGCAGATCACCCCACGAATGATGTGTG 2433
Db       2348 TCAACCAGACCACCTGCGAGAACCTCCTGCCGCAGCAGATCACGCCGCGCATGATGTGCG 2407

Qy       2434 TGGGTTTCCTCAGTGGGGGTGTGGACTCCTGCCAGGGTGACTCTGGTGGCCCCTTGTCAA 2493
Db       2408 TGGGCTTCCTCAGCGGCGGCGTGGACTCCTGCCAGGGTGATTCCGGGGGACCCCTGTCCA 2467

Qy       2494 GCGCGGAGAAAGATGGGCGAATGTTCCAGGCTGGTGTGGTGAGCTGGGGTGAAGGCTGCG 2553
Db       2468 GCGTGGAGGCGGATGGGCGGATCTTCCAGGCCGGTGTGGTGAGCTGGGGAGACGGCTGCG 2527

Qy       2554 CTCAGAGGAACAAGCCAGGCGTGTACACAAGGCTCCCTGTAGTTCGGGACTGGATCAAAG 2613
Db       2528 CTCAGAGGAACAAGCCAGGCGTGTACACAAGGCTCCCTCTGTTTCGGGACTGGATCAAAG 2587

Qy       2614 AGCACACTGGGGTATAGCAGCATGGACAGACA 2645
Db       2588 AGAACACTGGGGTATAGGGGCCGGGGCACCCA 2619
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RESULT 4
AAX87815
ID AAX87815 standard; cDNA; 3147 BP.
XX
AC AAX87815;
XX
DT 09-NOV-1999 (first entry)
XX
DE Tumour antigen derived gene-15 (TADG-15) cDNA.
XX
KW Tumour antigen derived gene-15; TADG-15; serine protease; human;
KW breast cancer; ovary cancer; carcinoma; diagnosis; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   23..2590
FT   /*tag= a
XX
PN WO9942120-A1.
XX
PD 26-AUG-1999.
XX
PF 18-FEB-1999; 99WO-US03436.
XX
PR 20-FEB-1998; 98US-0027337.
XX
PA (UYAR-) UNIV ARKANSAS.
XX
PI O'Brien TJ, Tanimoto H;
XX
DR WPI; 1999-527418/44.
DR P-PSDB; AAY06671.
XX
PT A new extracellular serine protease for diagnosis of neoplastic
PT disease
XX
PS Claim 2; Fig 9; 71pp; English.
XX
CC This is the nucleotide sequence of an isolated cDNA that codes for
CC an extracellular serine protease, termed tumour antigen derived
CC gene-15 protein (see AAY06671), that is overexpressed in breast and
CC ovarian carcinomas. The TADG-15 gene can be used as a diagnostic
CC and therapeutic target in ovarian carcinoma and other carcinomas
CC including breast, prostate, lung and colon. The TADG-15 cDNA was
CC isolated from ovarian carcinoma by PCR using primers directed to
CC conserved areas of the serine protease family. The invention
CC also provides: a vector that is capable of expressing DNA encoding
CC TADG-15 protein; host cells selected from bacterial cells
CC (especially Escherichia coli), mammalian cells, plant cells and
CC insect cells; and a method of detecting expression of TADG-15
CC protein using a hybridisation probe.
XX
SQ Sequence 3147 BP; 654 A; 952 C; 958 G; 583 T; 0 other;

Query Match 60.6%; Score 1883.2; DB 20; Length 3147;
Best Local Similarity 81.2%; Pred. No. 0;
Matches 2223; Conservative 0; Mismatches 508; Indels 5; Gaps 3;

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Db          5 GAGCGGCCTCGGGGTACCATGGGGAGCGATCGGGCCCGCAAGGGCGGAGGGGGCCCGAAG 64

Qy        105 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCTAGAGAACATGAATGGCTTTGAGGAG 164
Db         65 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCACGAGAAAGTGAATGGCTTGGAGGAA 124

Qy        165 GGTGTGGAGTTCCTGCCTGCGAACAATGCCAAGAAAGTGGAGAAGCGAGGCCCCAGGCGC 224
Db        125 GGCGTGGAGTTCCTGCCAGTCAACAACGTCAAGAAGGTGGAAAAGCATGGCCCGGGGCGC 184

Qy        225 TGGGTGGTGCTGGTGGCAGTGCTGTTCAGCTTCCTCTTGCTCTCCCTCATGGCTGGCTTG 284
Db        185 TGGGTGGTGCTGGCAGCCGTGCTGATCGGCCTCCTCTTGGTCTTGCTGGGGATCGGCTTC 244

Qy        285 CTGGTGTGGCACTTCCATTATCGGAATGTGCGGGTTCAAAAAGTCTTCAATGGCCATCTG 344
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Qy        345 AGGATCACAAATGAGATCTTTCTGGATGCGTATGAGAACTCCACCTCCACAGAGTTTATC 404
Db        305 AGGATCACAAATGAGAATTTTGTGGATGCCTACGAGAACTCCAACTCCACTGAGTTTGTA 364

Qy        405 AGCCTGGCCAGCCAGGTGAAGGAGGCGCTGAAGCTGCTGTACAATGAAGTCCCTGTCCTG 464
Db        365 AGCCTGGCCAGCAAGGTGAAGGACGCGCTGAAGCTGCTGTACAGCGGAGTCCCATTCCTG 424

Qy        465 GGTCCCTACCACAAGAAGTCGGCTGTAACTGCCTTCAGTGAGGGCAGTGTCATCGCCTAC 524
Db        425 GGCCCCTACCACAAGGAGTCGGCTGTGACGGCCTTCAGCGAGGGCAGCGTCATCGCCTAC 484

Qy        525 TACTGGTCAGAGTTCAGCATCCCCCCACACCTGGCAGAAGAGGTTGATCGCGCCATGGCT 584
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Qy        585 GTGGAGCGAGTTGTAACATTGCCACCCCGAGCACGGGCACTGAAATCCTTCGTGCTAACA 644
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Db        605 TCAGTGGTGGCTTTCCCCACGGACTCCAAAACAGTACAGAGGACCCAGGACAACAGCTGC 664

Qy        705 AGTTTTGCCCTGCATGCCCATGGTGCAGCAGTGACACGCTTCACTACCCCTGGCTTCCCC 764
Db        665 AGCTTTGGCCTGCACGCCCGCGGTGTGGAGCTGATGCGCTTCACCACGCCCGGCTTCCCT 724

Qy        765 AACAGTCCCTACCCGGCGCATGCCCGCTGCCAGTGGGTCCTGCGGGGGGACGCCGACTCT 824
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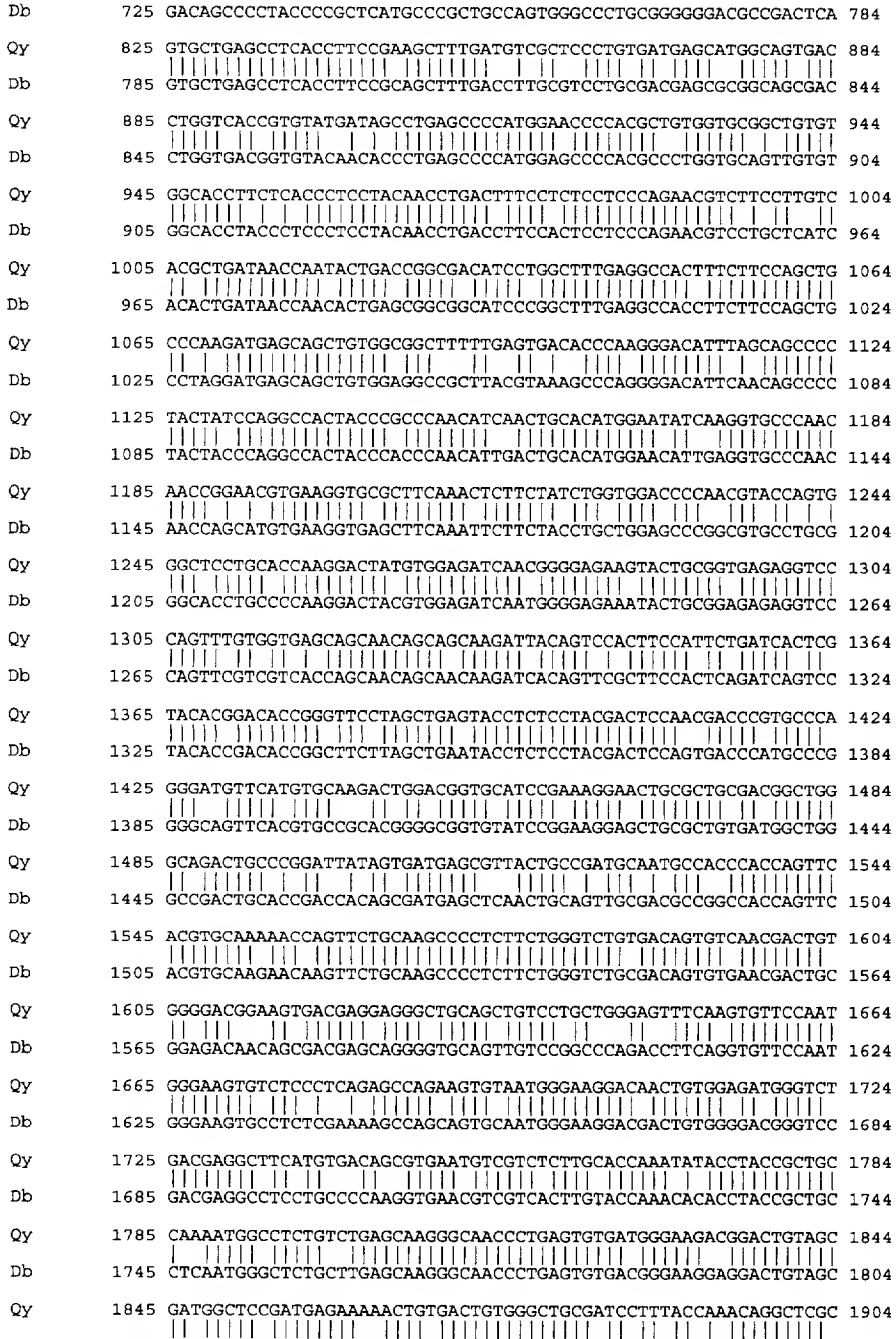

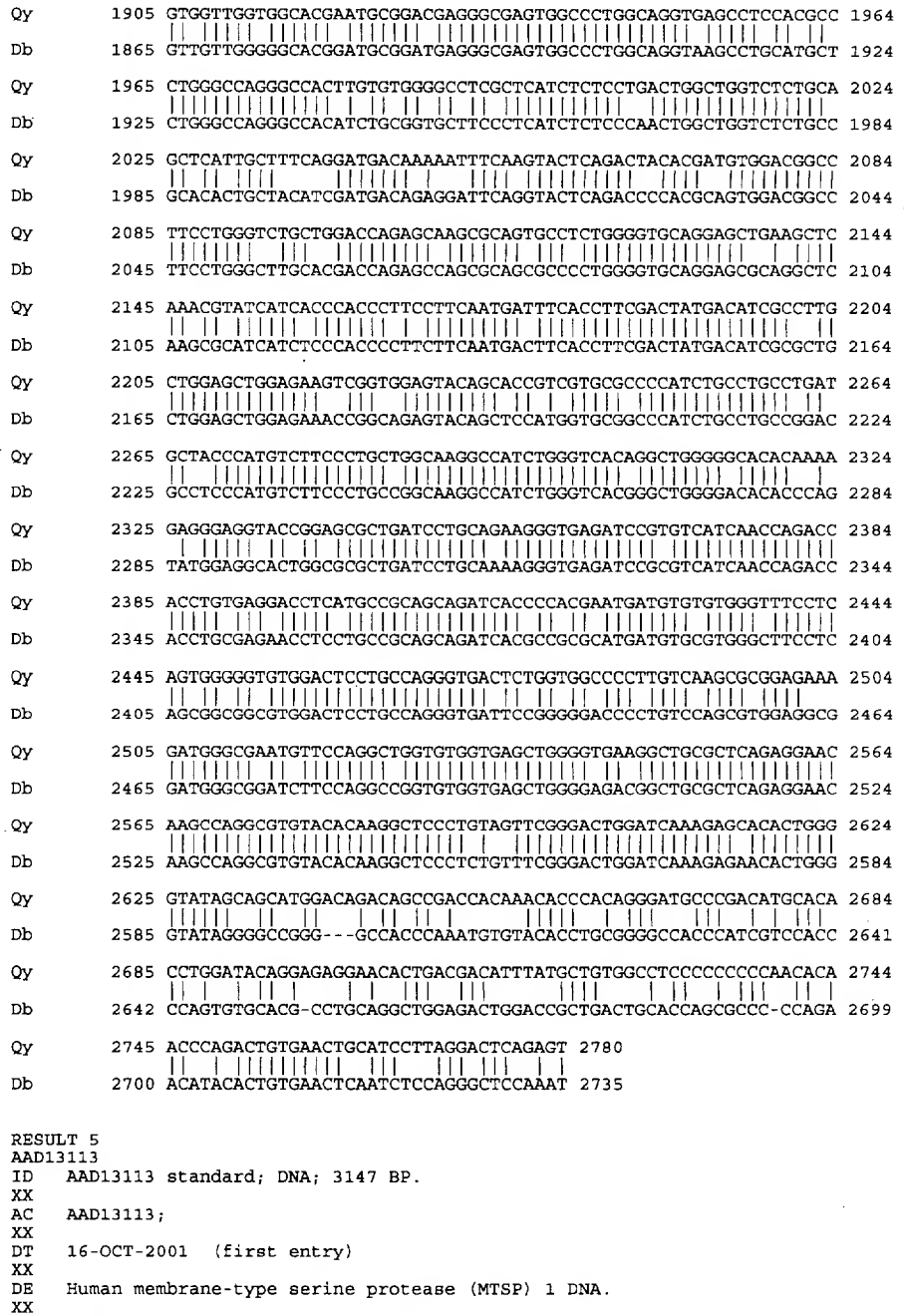

RESULT 5
AAD13113
ID AAD13113 standard; DNA; 3147 BP.
XX
AC AAD13113;
XX
DT 16-OCT-2001 (first entry)
XX
DE Human membrane-type serine protease (MTSP) 1 DNA.
XX
KW Human; transmembrane serine protease; membrane-type serine protease;

```
KW   MTSP; protease domain; neoplastic disease; tumour; cancer; cytostatic;
KW   lung carcinoma; colon adenocarcinoma; ovarian carcinoma; gene therapy;
KW   matriptase; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             23..2590
FT                   /*tag=  a
FT                   /product= "Human transmembrane serine protease (MTSP) 1"
XX
PN   WO200157194-A2.
XX
PD   09-AUG-2001.
XX
PF   02-FEB-2001; 2001WO-US03471.
XX
PR   03-FEB-2000; 2000US-0179982.
PR   18-FEB-2000; 2000US-0183542.
PR   22-JUN-2000; 2000US-0213124.
PR   26-JUL-2000; 2000US-0220970.
PR   08-SEP-2000; 2000US-0657986.
PR   22-SEP-2000; 2000US-0234840.
XX
PA   (CORV-) CORVAS INT INC.
XX
PI   Madison EL,  Ong EO,  Yeh J;
XX
DR   WPI; 2001-488877/53.
DR   P-PSDB; AAE06930.
XX
PT   Novel single chain polypeptide comprising protease domain of type-II
PT   membrane-type serine protease or its catalytically active portion
PT   useful for treating and preventing cancer and tumor  -
XX
PS   Claim 14; Page 191-195; 256pp; English.
XX
CC   The invention relates to transmembrane serine proteases and their
CC   corresponding nucleotides and the protease domain of a type-II
CC   membrane-type serine protease (MTSP). MTSP is useful for identifying
CC   compounds that modulate or inhibits its proteolytic activity and for
CC   formulating a medicament for treating neoplastic disease. MTSP and
CC   its corresponding nucleotides are useful in preventing or treating
CC   tumours or cancers such as lung carcinoma, colon adenocarcinoma and
CC   ovarian carcinoma, in diagnostics and in hybridisation assays. MTSP
CC   is useful as a diagnostic marker for tumour development, growth and/or
CC   progression and as immunogens to generate antibodies that specifically
CC   bind to it. MTSP DNA is useful in a yeast two-hybrid system and in
CC   gene therapy. The present sequence is a DNA encoding human MTSP1
CC   protein (also called matriptase).
XX
SQ   Sequence 3147 BP; 654 A; 952 C; 958 G; 583 T; 0 other;

  Query Match           60.6%;  Score 1883.2;  DB 22;  Length 3147;
  Best Local Similarity  81.2%;  Pred. No. 0;
  Matches 2223;  Conservative    0;  Mismatches  508;  Indels    5;  Gaps    3;

Qy         45 GATCGGACCGCCAAAACCATGGGTAGCAATCGGGGCCGCAAGGCCGGAGGGGGCTCTCAG 104
              ||  |||  |       |||||||| ||| ||||||  |||||||| ||||||||| |  ||
Db          5 GAGCGGCCTCGGGGTACCATGGGGAGCGATCGGGCCCGCAAGGGCGGAGGGGGCCCGAAG  64

Qy        105 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCTAGAGAACATGAATGGCTTTGAGGAG 164
              |||||||||||||||||||||||||||||||||  |||||  |||||||||| |||||
Db         65 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCACGAGAAAGTGAATGGCTTGGAGGAA 124

Qy        165 GGTGTGGAGTTCCTGCCTGCGAACAATGCCAAGAAAGTGGAGAAGCGAGGCCCCAGGCGC 224
              ||  |||||||||||||  |  |||||  | ||||||  |||||  ||||  |||||  |||||
Db        125 GGCGTGGAGTTCCTGCCAGTCAACAACGTCAAGAAGGTGGAAAAGCATGGCCCGGGGCGC 184

Qy        225 TGGGTGGTGCTGGTGGCAGTGCTGTTCAGCTTCCTCTTGCTCTCCCTCATGGCTGGCTTG 284
              ||||||||||||  ||  ||||||  ||  ||  ||||||||  |||  ||    |  |||||
Db        185 TGGGTGGTGCTGGCAGCCGTGCTGATCGGCCTCCTCTTGGTCTTGCTGGGGATCGGCTTC 244

Qy        285 CTGGTGTGGCACTTCCATTATCGGAATGTGCGGGTTCAAAAAGTCTTCAATGGCCATCTG 344
              ||||||||||  ||  ||  |||  |  |||||  ||  ||  ||  ||||||||||  |  ||
Db        245 CTGGTGTGGCATTTGCAGTACCGGGACGTGCGTGTCCAGAAGGTCTTCAATGGCTACATG 304

Qy        345 AGGATCACAAATGAGATCTTTCTGGATGCGTATGAGAACTCCACCTCCACAGAGTTTATC 404
              ||||||||||||||||  |||  |||||||  ||  |||||||||  ||||||  ||||||  |
Db        305 AGGATCACAAATGAGAATTTTGTGGATGCCTACGAGAACTCCAACTCCACTGAGTTTGTA 364

Qy        405 AGCCTGGCCAGCCAGGTGAAGGAGGCGCTGAAGCTGCTGTACAATGAAGTCCCTGTCCTG 464
              ||||||||||||  ||||||||||  ||||||||||||||||||||  |  ||||||  |||||
Db        365 AGCCTGGCCAGCAAGGTGAAGGACGCGCTGAAGCTGCTGTACAGCGGAGTCCCATTCCTG 424

Qy        465 GGTCCCTACCACAAGAAGTCGGCTGTAACTGCCTTCAGTGAGGGCAGTGTCATCGCCTAC 524
              ||  ||||||||||||  ||||||||||  ||  ||||||||  ||||||||  ||||||||||
Db        425 GGCCCCTACCACAAGGAGTCGGCTGTGACGGCCTTCAGCGAGGGCAGCGTCATCGCCTAC 484

Qy        525 TACTGGTCAGAGTTCAGCATCCCCCCACACCTGGCAGAAGAGGTTGATCGCGCCATGGCT 584
              ||||||||  ||||||||||||||  |  |||||||  ||  ||||  ||  ||||  ||||||
Db        485 TACTGGTCTGAGTTCAGCATCCCGCAGCACCTGGTGGAGGAGGCCGAGCGCGTCATGGCC 544

Qy        585 GTGGAGCGAGTTGTAACATTGCCACCCCGAGCACGGGCACTGAAATCCTTCGTGCTAACA 644
              |  ||||||  ||  ||  |    ||||  ||  ||  ||  ||  |  |||||  |||||  |||  |  ||
Db        545 GAGGAGCGCGTAGTCATGCTGCCCCCGCGGGCGCGCTCCCTGAAGTCCTTTGTGGTCACC 604

Qy        645 TCTGTGGTGGCCTTCCCCATTGACCCCAGAATGCTGCAGAGGACTCAGGACAACAGCTGC 704
              ||  ||||||||  |||||||  |||  |||  ||    |  ||||||||  ||||||||||||||
Db        605 TCAGTGGTGGCTTTCCCCACGGACTCCAAAACAGTACAGAGGACCCAGGACAACAGCTGC 664

Qy        705 AGTTTTGCCCTGCATGCCCATGGTGCAGCAGTGACACGCTTCACTACCCCTGGCTTCCCC 764
              ||  ||||  ||||||  ||||  ||||  |  |||  ||||||||  ||  ||  ||||||||
Db        665 AGCTTTGGCCTGCACGCCCGCGGTGTGGAGCTGATGCGCTTCACCACGCCCGGCTTCCCT 724

Qy        765 AACAGTCCCTACCCGGCGCATGCCCGCTGCCAGTGGGTCCTGCGGGGGGGACGCCGACTCT 824
              ||||  ||||||||  ||  ||||||||||||||||||  ||||||||||||||||||||
Db        725 GACAGCCCCTACCCCGCTCATGCCCGCTGCCAGTGGGCCCTGCGGGGGGGACGCCGACTCA 784

Qy        825 GTGCTGAGCCTCACCTTCCGAAGCTTTGATGTCGCTCCCTGTGATGAGCATGGCAGTGAC 884
              ||||||||||||||||||||  ||||||||  |  ||  ||||  ||  ||||  |||||  |||
Db        785 GTGCTGAGCCTCACCTTCCGCAGCTTTGACCTTGCGTCCTGCGACGAGCGCGGCAGCGAC 844

Qy        885 CTGGTCACCGTGTATGATAGCCTGAGCCCCATGGAACCCCACGCTGTGGTGCGGCTGTGT 944
              |||||  ||  |||||  |  |  ||||||||||||||  |||||||  ||||||  |  |||||
Db        845 CTGGTGACGGTGTACAACACCCTGAGCCCCATGGAGCCCCACGCCCTGGTGCAGTTGTGT 904

Qy        945 GGCACCTTCTCACCCTCCTACAACCTGACTTTCCTCTCCTCCCAGAACGTCTTCCTTGTC 1004
              |||||||  |  ||||||||||||||||  ||||  ||||||||||||||  |  ||  ||
Db        905 GGCACCTACCCTCCCTCCTACAACCTGACCTTCCACTCCTCCCAGAACGTCCTGCTCATC 964

Qy       1005 ACGCTGATAACCAATACTGACCGGCGACATCCTGGCTTTGAGGCCACTTTCTTCCAGCTG 1064
              ||  ||||||||||  |||||  |||||  ||||  ||||||||||||  |||||||||||
Db        965 ACACTGATAACCAACACTGAGCGGCGGCATCCCGGCTTTGAGGCCACCTTCTTCCAGCTG 1024

Qy       1065 CCCAAGATGAGCAGCTGTGGCGGCTTTTTGAGTGACACCCAAGGGACATTTAGCAGCCCC 1124
              ||  |  ||||||||||||||||  |||    ||  ||  |  ||||  ||||||||  |  |||||||
Db       1025 CCTAGGATGAGCAGCTGTGGAGGCCGCTTACGTAAAGCCCAGGGGACATTCAACAGCCCC 1084

Qy       1125 TACTATCCAGGCCACTACCCGCCCAACATCAACTGCACATGGAATATCAAGGTGCCCAAC 1184
              |||||  ||||||||||||||  |||||||  ||||||||||||  ||  ||||||||||
Db       1085 TACTACCCAGGCCACTACCCACCCAACATTGACTGCACATGGAACATTGAGGTGCCCAAC 1144

Qy       1185 AACCGGAACGTGAAGGTGCGCTTCAAACTCTTCTATCTGGTGGACCCCAACGTACCAGTG 1244
              ||||  |  |||||||||  |||||||  ||||||  |||  ||||  |||  ||  |  |
Db       1145 AACCAGCATGTGAAGGTGAGCTTCAAATTCTTCTACCTGCTGGAGCCCGGCGTGCCTGCG 1204

Qy       1245 GGCTCCTGCACCAAGGACTATGTGGAGATCAACGGGGAGAAGTACTGCGGTGAGAGGTCC 1304
              |||  |||||  ||||||||||  ||||||||||  ||||||||  ||||||||  |||||||||
Db       1205 GGCACCTGCCCCAAGGACTACGTGGAGATCAATGGGGAGAAATACTGCGGAGAGAGGTCC 1264

Qy       1305 CAGTTTGTGGTGAGCAGCAACAGCAGCAAGATTACAGTCCACTTCCATTCTGATCACTCG 1364
              |||||  ||  ||  |  ||||||||||  ||||||  |||||  |  ||||||  ||  |||||  ||
Db       1265 CAGTTCGTCGTCACCAGCAACAGCAACAAGATCACAGTTCGCTTCCACTCAGATCAGTCC 1324

Qy       1365 TACACGGACACCGGGTTCCTAGCTGAGTACCTCTCCTACGACTCCAACGACCCGTGCCCA 1424
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Db       1325 TACACCGACACCGGCTTCTTAGCTGAATACCTCTCCTACGACTCCAGTGACCCATGCCCG 1384

Qy       1425 GGGATGTTCATGTGCAAGACTGGACGGTGCATCCGAAAGGAACTGCGCTGCGACGGCTGG 1484

Db       1385 GGGCAGTTCACGTGCCGCACGGGGCGGTGTATCCGGAAGGAGCTGCGCTGTGATGGCTGG 1444

Qy       1485 GCAGACTGCCCGGATTATAGTGATGAGCGTTACTGCCGATGCAATGCCACCCACCAGTTC 1544

Db       1445 GCCGACTGCACCGACCACAGCGATGAGCTCAACTGCAGTTGCGACGCCGGCCACCAGTTC 1504

Qy       1545 ACGTGCAAAAACCAGTTCTGCAAGCCCCTCTTCTGGGTCTGTGACAGTGTCAACGACTGT 1604

Db       1505 ACGTGCAAGAACAAGTTCTGCAAGCCCCTCTTCTGGGTCTGCGACAGTGTGAACGACTGC 1564

Qy       1605 GGGGACGGAAGTGACGAGGAGGGCTGCAGCTGTCCTGCTGGGAGTTTCAAGTGTTCCAAT 1664

Db       1565 GGAGACAACAGCGACGAGCAGGGGTGCAGTTGTCCGGCCCAGACCTTCAGGTGTTCCAAT 1624

Qy       1665 GGGAAGTGTCTCCCTCAGAGCCAGAAGTGTAATGGGAAGGACAACTGTGGAGATGGGTCT 1724

Db       1625 GGGAAGTGCCTCTCGAAAAGCCAGCAGTGCAATGGGAAGGACGACTGTGGGGACGGGTCC 1684

Qy       1725 GACGAGGCTTCATGTGACAGCGTGAATGTCGTCTCTTGCACCAAATATACCTACCGCTGC 1784

Db       1685 GACGAGGCCTCCTGCCCCAAGGTGAACGTCGTCACTTGTACCAAACACACCTACCGCTGC 1744

Qy       1785 CAAAATGGCCTCTGTCTGAGCAAGGGCAACCCTGAGTGTGATGGGAAGACGGACTGTAGC 1844

Db       1745 CTCAATGGGCTCTGCTTGAGCAAGGGCAACCCTGAGTGTGACGGGAAGGAGGACTGTAGC 1804

Qy       1845 GATGGCTCCGATGAGAAAAACTGTGACTGTGGGCTGCGATCCTTTACCAAACAGGCTCGC 1904

Db       1805 GACGGCTCAGATGAGAAGGACTGCGACTGTGGGCTGCGGTCATTCACGAGACAGGCTCGT 1864

Qy       1905 GTGGTTGGTGGCACGAATGCGGACGAGGGCGAGTGGCCCTGGCAGGTGAGCCTCCACGCC 1964

Db       1865 GTTGTTGGGGGCACGGATGCGGATGAGGGCGAGTGGCCCTGGCAGGTAAGCCTGCATGCT 1924

Qy       1965 CTGGGCCAGGGCCACTTGTGTGGGGCCTCGCTCATCTCTCCTGACTGGCTGGTCTCTGCA 2024

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Qy       2025 GCTCATTGCTTTCAGGATGACAAAAATTTCAAGTACTCAGACTACACGATGTGGACGGCC 2084

Db       1985 GCACACTGCTACATCGATGACAGAGGATTCAGGTACTCAGACCCCACGCAGTGGACGGCC 2044

Qy       2085 TTCCTGGGTCTGCTGGACCAGAGCAAGCGCAGTGCCTCTGGGGTGCAGGAGCTGAAGCTC 2144

Db       2045 TTCCTGGGCTTGCACGACCAGAGCCAGCGCAGCGCCCCTGGGGTGCAGGAGCGCAGGCTC 2104

Qy       2145 AAACGTATCATCACCCACCCTTCCTTCAATGATTTCACCTTCGACTATGACATCGCCTTG 2204

Db       2105 AAGCGCATCATCTCCCACCCCTTCTTCAATGACTTCACCTTCGACTATGACATCGCGCTG 2164

Qy       2205 CTGGAGCTGGAGAAGTCGGTGGAGTACAGCACCGTCGTGCGCCCCATCTGCCTGCCTGAT 2264

Db       2165 CTGGAGCTGGAGAAACCGGCAGAGTACAGCTCCATGGTGCGGCCCATCTGCCTGCCGGAC 2224

Qy       2265 GCTACCCATGTCTTCCCTGCTGGCAAGGCCATCTGGGTCACAGGCTGGGGGCACACAAAA 2324

Db       2225 GCCTCCCATGTCTTCCCTGCCGGCAAGGCCATCTGGGTCACGGGCTGGGGACACACCCAG 2284

Qy       2325 GAGGGAGGTACCGGAGCGCTGATCCTGCAGAAGGGTGAGATCCGTGTCATCAACCAGACC 2384

Db       2285 TATGGAGGCACTGGCGCGCTGATCCTGCAAAAGGGTGAGATCCGCGTCATCAACCAGACC 2344

Qy       2385 ACCTGTGAGGACCTCATGCCGCAGCAGATCACCCCACGAATGATGTGTGTGGGTTTCCTC 2444

Db       2345 ACCTGCGAGAACCTCCTGCCGCAGCAGATCACGCCGCGCATGATGTGCGTGGGCTTCCTC 2404

Qy       2445 AGTGGGGGTGTGGACTCCTGCCAGGGTGACTCTGGTGGCCCCTTGTCAAGCGCGGAGAAA 2504

Db       2405 AGCGGCGGCGTGGACTCCTGCCAGGGTGATTCCGGGGGACCCCTGTCCAGCGTGGAGGCG 2464

Qy       2505 GATGGGCGAATGTTCCAGGCTGGTGTGGTGAGCTGGGGTGAAGGCTGCGCTCAGAGGAAC 2564

Db       2465 GATGGGCGGATCTTCCAGGCCGGTGTGGTGAGCTGGGGAGACGGCTGCGCTCAGAGGAAC 2524

Qy       2565 AAGCCAGGCGTGTACACAAGGCTCCCTGTAGTTCGGGACTGGATCAAAGAGCACACTGGG 2624

Db       2525 AAGCCAGGCGTGTACACAAGGCTCCCTCTGTTTCGGGACTGGATCAAAGAGAACACTGGG 2584

Qy       2625 GTATAGCAGCATGGACAGACAGCCGACCACAAACACCCACAGGGATGCCCGACATGCACA 2684

Db       2585 GTATAGGGGCCGGG---GCCACCCAAATGTGTACACCTGCGGGGCCACCCATCGTCCACC 2641

Qy       2685 CCTGGATACAGGAGAGGAACACTGACGACATTTATGCTGTGGCCTCCCCCCCCCCAACACA 2744

Db       2642 CCAGTGTGCACG-CCTGCAGGCTGGAGACTGGACCGCTGACTGCACCAGCGCCC-CCAGA 2699

Qy       2745 ACCCAGACTGTGAACTGCATCCTTAGGACTCAGAGT 2780

Db       2700 ACATACACTGTGAACTCAATCTCCAGGGCTCCAAAT 2735
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RESULT 6
AAD13155

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ID   AAD13155 standard; DNA; 3147 BP.
XX
AC   AAD13155;
XX
DT   16-OCT-2001  (first entry)
XX
DE   Human membrane-type serine protease (MTSP) 1 protease domain DNA.
XX
KW   Human; transmembrane serine protease; membrane-type serine protease;
KW   MTSP; protease domain; neoplastic disease; tumour; cancer; cytostatic;
KW   lung carcinoma; colon adenocarcinoma; ovarian carcinoma; gene therapy;
KW   matriptase; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1865..2590
FT                   /*tag=  a
FT                   /product= "Human transmembrane serine protease
FT                   (MTSP) 1 protease domain"
FT                   /note= "CDS does not include start codon"
FT                   /partial
XX
PN   WO200157194-A2.
XX
PD   09-AUG-2001.
XX
PF   02-FEB-2001; 2001WO-US03471.
XX
PR   03-FEB-2000; 2000US-0179982.
PR   18-FEB-2000; 2000US-0183542.
PR   22-JUN-2000; 2000US-0213124.
PR   26-JUL-2000; 2000US-0220970.
PR   08-SEP-2000; 2000US-0657986.
PR   22-SEP-2000; 2000US-0234840.
XX
PA   (CORV-) CORVAS INT INC.
XX
PI   Madison EL,  Ong EO,  Yeh J;
XX
DR   WPI; 2001-488877/53.
DR   P-PSDB; AAE06936.
XX
PT   Novel single chain polypeptide comprising protease domain of type-II
PT   membrane-type serine protease or its catalytically active portion
PT   useful for treating and preventing cancer and tumor  -
XX
PS   Example 6; Page 225-227; 256pp; English.
```

XX
CC The invention relates to transmembrane serine proteases and their
CC corresponding nucleotides and the protease domain of a type-II
CC membrane-type serine protease (MTSP). MTSP is useful for identifying
CC compounds that modulate or inhibits its proteolytic activity and for
CC formulating a medicament for treating neoplastic disease. MTSP and
CC its corresponding nucleotides are useful in preventing or treating
CC tumours or cancers such as lung carcinoma, colon adenocarcinoma and
CC ovarian carcinoma, in diagnostics and in hybridisation assays. MTSP
CC is useful as a diagnostic marker for tumour development, growth and/or
CC progression and as immunogens to generate antibodies that specifically
CC bind to it. MTSP DNA is useful in a yeast two-hybrid system and in
CC gene therapy. The present sequence is a DNA encoding protease domain of
CC human MTSP1 protein (also called matriptase).
XX
SQ Sequence 3147 BP; 654 A; 952 C; 958 G; 583 T; 0 other;

Query Match 60.6%; Score 1883.2; DB 22; Length 3147;
Best Local Similarity 81.2%; Pred. No. 0;
Matches 2223; Conservative 0; Mismatches 508; Indels 5; Gaps 3;

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Qy        45 GATCGGACCGCCAAAACCATGGGTAGCAATCGGGGCCGCAAGGCCGGAGGGGGCTCTCAG 104
             || ||| |       |||||||| ||| |||||| |||||||| ||||||||| |   ||
Db         5 GAGCGGCCTCGGGGTACCATGGGGAGCGATCGGGCCCGCAAGGGCGGAGGGGGCCCGAAG 64

Qy       105 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCTAGAGAACATGAATGGCTTTGAGGAG 164
             ||||||||||||||||||||||||||||||||  |||||  |||||||||| |||||
Db        65 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCACGAGAAAGTGAATGGCTTGGAGGAA 124

Qy       165 GGTGTGGAGTTCCTGCCTGCGAACAATGCCAAGAAAGTGGAGAAGCGAGGCCCCAGGCGC 224
             || |||||||||||| |  |||||  | ||||||  |||||  ||||  |||||  |||||
Db       125 GGCGTGGAGTTCCTGCCAGTCAACAACGTCAAGAAGGTGGAAAAGCATGGCCCGGGGCGC 184

Qy       225 TGGGTGGTGCTGGTGGCAGTGCTGTTCAGCTTCCTCTTGCTCTCCCTCATGGCTGGCTTG 284
             ||||||||||||  || ||||||  || || ||||||||  |||  ||    |  |||||
Db       185 TGGGTGGTGCTGGCAGCCGTGCTGATCGGCCTCCTCTTGGTCTTGCTGGGGATCGGCTTC 244

Qy       285 CTGGTGTGGCACTTCCATTATCGGAATGTGCGGGTTCAAAAAGTCTTCAATGGCCATCTG 344
             ||||||||||| || || || ||| | ||||| || || || ||||||||||| |  ||
Db       245 CTGGTGTGGCATTTGCAGTACCGGGACGTGCGTGTCCAGAAGGTCTTCAATGGCTACATG 304

Qy       345 AGGATCACAAATGAGATCTTTCTGGATGCGTATGAGAACTCCACCTCCACAGAGTTTATC 404
             |||||||||||||||  ||| |||||| || |||||||||  |||||  ||||||  |
Db       305 AGGATCACAAATGAGAATTTTGTGGATGCCTACGAGAACTCCAACTCCACTGAGTTTGTA 364

Qy       405 AGCCTGGCCAGCCAGGTGAAGGAGGCGCTGAAGCTGCTGTACAATGAAGTCCCTGTCCTG 464
             |||||||||||  |||||||||  ||||||||||||||||||  | ||||||  |||||
Db       365 AGCCTGGCCAGCAAGGTGAAGGACGCGCTGAAGCTGCTGTACAGCGGAGTCCCATTCCTG 424

Qy       465 GGTCCCTACCACAAGAAGTCGGCTGTAACTGCCTTCAGTGAGGGCAGTGTCATCGCCTAC 524
             || |||||||||||  ||||||||||  || ||||||||  ||||||||  ||||||||||||
Db       425 GGCCCCTACCACAAGGAGTCGGCTGTGACGGCCTTCAGCGAGGGCAGCGTCATCGCCTAC 484

Qy       525 TACTGGTCAGAGTTCAGCATCCCCCCACACCTGGCAGAAGAGGTTGATCGCGCCATGGCT 584
             ||||||||  ||||||||||||||  |||||||  ||  ||||  ||  |||| ||||||
Db       485 TACTGGTCTGAGTTCAGCATCCCGCAGCACCTGGTGGAGGAGGCCGAGCGCGTCATGGCC 544

Qy       585 GTGGAGCGAGTTGTAACATTGCCACCCCGAGCACGGGCACTGAAATCCTTCGTGCTAACA 644
             | ||||||  ||  || |   ||||  ||  ||  ||  | |||||  |||||  ||| | ||
Db       545 GAGGAGCGCGTAGTCATGCTGCCCCCGCGGGCGCGCTCCCTGAAGTCCTTTGTGGTCACC 604

Qy       645 TCTGTGGTGGCCTTCCCCATTGACCCCAGAATGCTGCAGAGGACTCAGGACAACAGCTGC 704
             ||  |||||||  |||||||  |||  |||  ||    | ||||||||  ||||||||||||||
Db       605 TCAGTGGTGGCTTTCCCCACGGACTCCAAAACAGTACAGAGGACCCAGGACAACAGCTGC 664

Qy       705 AGTTTTGCCCTGCATGCCCATGGTGCAGCAGTGACACGCTTCACTACCCCTGGCTTCCCC 764
             ||  ||||  ||||||  |||  ||||  |  |||  ||||||||  ||  ||||||||||
Db       665 AGCTTTGGCCTGCACGCCCGCGGTGTGGAGCTGATGCGCTTCACCACGCCCGGCTTCCCT 724

Qy       765 AACAGTCCCTACCCGGCGCATGCCCGCTGCCAGTGGGTCCTGCGGGGGGACGCCGACTCT 824
               ||||  ||||||||  ||  ||||||||||||||||||  ||||||||||||||||||||
Db       725 GACAGCCCCTACCCCGCTCATGCCCGCTGCCAGTGGGCCCTGCGGGGGGACGCCGACTCA 784

Qy       825 GTGCTGAGCCTCACCTTCCGAAGCTTTGATGTCGCTCCCTGTGATGAGCATGGCAGTGAC 884
             |||||||||||||||||||  ||||||||  | ||  |||| ||  ||||  ||||| |||
Db       785 GTGCTGAGCCTCACCTTCCGCAGCTTTGACCTTGCGTCCTGCGACGAGCGCGGCAGCGAC 844

Qy       885 CTGGTCACCGTGTATGATAGCCTGAGCCCCATGGAACCCCACGCTGTGGTGCGGCTGTGT 944
             |||||  ||  |||||  |  | ||||||||||||||  ||||||||  ||||||  | |||||
Db       845 CTGGTGACGGTGTACAACACCCTGAGCCCCATGGAGCCCCACGCCCTGGTGCAGTTGTGT 904

Qy       945 GGCACCTTCTCACCCTCCTACAACCTGACTTTCCTCTCCTCCCAGAACGTCTTCCTTGTC 1004
             |||||||  |  ||||||||||||||||||  ||||  ||||||||||||||||  |  ||  ||
Db       905 GGCACCTACCCTCCCTCCTACAACCTGACCTTCCACTCCTCCCAGAACGTCCTGCTCATC 964

Qy      1005 ACGCTGATAACCAATACTGACCGGCGACATCCTGGCTTTGAGGCCACTTTCTTCCAGCTG 1064
             ||  ||||||||||  |||||  |||||  |||||||||||||||  ||||||||||
Db       965 ACACTGATAACCAACACTGAGCGGCGGCATCCCGGCTTTGAGGCCACCTTCTTCCAGCTG 1024

Qy      1065 CCCAAGATGAGCAGCTGTGGCGGCTTTTTGAGTGACACCCAAGGGACATTTAGCAGCCCC 1124
             ||  | ||||||||||||||||  |||  ||  ||  |  ||||  ||||||||  | |||||||
Db      1025 CCTAGGATGAGCAGCTGTGGAGGCCGCTTACGTAAAGCCCAGGGGACATTCAACAGCCCC 1084

Qy      1125 TACTATCCAGGCCACTACCCGCCCAACATCAACTGCACATGGAATATCAAGGTGCCCAAC 1184
             |||||  ||||||||||||||  ||||||||  ||||||||||||  ||  ||||||||||||
Db      1085 TACTACCCAGGCCACTACCCACCCAACATTGACTGCACATGGAACATTGAGGTGCCCAAC 1144

Qy      1185 AACCGGAACGTGAAGGTGCGCTTCAAACTCTTCTATCTGGTGGACCCCAACGTACCAGTG 1244
             |||| | | |||||||||  |||||||  ||| |||| |||  ||| || | |
Db      1145 AACCAGCATGTGAAGGTGAGCTTCAAATTCTTCTACCTGCTGGAGCCCGGCGTGCCTGCG 1204

Qy      1245 GGCTCCTGCACCAAGGACTATGTGGAGATCAACGGGGAGAAGTACTGCGGTGAGAGGTCC 1304
             |||  |||||  ||||||||||  ||||||||||  ||||||||  ||||||||  |||||||||
Db      1205 GGCACCTGCCCCAAGGACTACGTGGAGATCAATGGGGAGAAATACTGCGGAGAGAGGTCC 1264

Qy      1305 CAGTTTGTGGTGAGCAGCAACAGCAGCAAGATTACAGTCCACTTCCATTCTGATCACTCG 1364
             |||||  ||  ||  |  ||||||||||  ||||||  |||||  |  ||||||  ||  |||||  ||
Db      1265 CAGTTCGTCGTCACCAGCAACAGCAACAAGATCACAGTTCGCTTCCACTCAGATCAGTCC 1324

Qy      1365 TACACGGACACCGGGTTCCTAGCTGAGTACCTCTCCTACGACTCCAACGACCCGTGCCCA 1424
             |||||  |||||||||  |||  |||||||  ||||||||||||||||||||  |||||  |||||
Db      1325 TACACCGACACCGGCTTCTTAGCTGAATACCTCTCCTACGACTCCAGTGACCCATGCCCG 1384

Qy      1425 GGGATGTTCATGTGCAAGACTGGACGGTGCATCCGAAAGGAACTGCGCTGCGACGGCTGG 1484
             |||  |||||  ||||    ||  ||  |||||  |||||  |||||  ||||||||  ||  ||||||
Db      1385 GGGCAGTTCACGTGCCGCACGGGGCGGTGTATCCGGAAGGAGCTGCGCTGTGATGGCTGG 1444

Qy      1485 GCAGACTGCCCCGGATTATAGTGATGAGCGTTACTGCCGATGCAATGCCACCCACCAGTTC 1544
             ||  ||||||  |  ||  |  ||  |||||||  |||||  |  |||  |  |||  ||||||||||
Db      1445 GCCGACTGCACCGACCACAGCGATGAGCTCAACTGCAGTTGCGACGCCGGCCACCAGTTC 1504

Qy      1545 ACGTGCAAAAACCAGTTCTGCAAGCCCCTCTTCTGGGTCTGTGACAGTGTCAACGACTGT 1604
             ||||||||  |||  ||||||||||||||||||||||||||||||||  ||||||||  ||||||||
Db      1505 ACGTGCAAGAACAAGTTCTGCAAGCCCCTCTTCTGGGTCTGCGACAGTGTGAACGACTGC 1564

Qy      1605 GGGGACGGAAGTGACGAGGAGGGCTGCAGCTGTCCTGCTGGGAGTTTCAAGTGTTCCAAT 1664
             ||  |||    ||  ||||||  ||||  |||||  |||||  ||    ||  ||||  ||||||||||
Db      1565 GGAGACAACAGCGACGAGCAGGGGTGCAGTTGTCCGGCCCAGACCTTCAGGTGTTCCAAT 1624

Qy      1665 GGGAAGTGTCTCCCTCAGAGCCAGAAGTGTAATGGGAAGGACAACTGTGGAGATGGGTCT 1724
             ||||||||  |||  |  ||||||  ||||  ||||||||||||  ||||||  ||  |||||
Db      1625 GGGAAGTGCCTCTCGAAAAGCCAGCAGTGCAATGGGAAGGACGACTGTGGGGACGGGTCC 1684

Qy      1725 GACGAGGCTTCATGTGACAGCGTGAATGTCGTCTCTTGCACCAAATATACCTACCGCTGC 1784
             ||||||||  ||  ||    ||  |||||  ||||  ||||||  |  ||||||||||||
Db      1685 GACGAGGCCTCCTGCCCCAAGGTGAACGTCGTCACTTGTACCAAACACACCTACCGCTGC 1744

Qy      1785 CAAAATGGCCTCTGTCTGAGCAAGGGCAACCCTGAGTGTGATGGGAAGACGGACTGTAGC 1844
             |  |||||  |||||  ||||||||||||||||||||||||||  ||||||  ||||||||||
Db      1745 CTCAATGGGCTCTGCTTGAGCAAGGGCAACCCTGAGTGTGACGGGAAGGAGGACTGTAGC 1804

Qy      1845 GATGGCTCCGATGAGAAAAAACTGTGACTGTGGGCTGCGATCCTTTACCAAACAGGCTCGC 1904
             ||  |||||  ||||||||  ||||  ||||||||||||||  ||  ||  ||  |||||||||
Db      1805 GACGGCTCAGATGAGAAGGACTGCGACTGTGGGCTGCGGTCATTCACGAGACAGGCTCGT 1864

Qy      1905 GTGGTTGGTGGCACGAATGCGGACGAGGGCGAGTGGCCCTGGCAGGTGAGCCTCCACGCC 1964
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Db       1865 GTTGTTGGGGGCACGGATGCGGATGAGGGCGAGTGGCCCTGGCAGGTAAGCCTGCATGCT 1924

Qy       1965 CTGGGCCAGGGCCACTTGTGTGGGGCCTCGCTCATCTCTCCTGACTGGCTGGTCTCTGCA 2024

Db       1925 CTGGGCCAGGGCCACATCTGCGGTGCTTCCCTCATCTCTCCCAACTGGCTGGTCTCTGCC 1984

Qy       2025 GCTCATTGCTTTCAGGATGACAAAAATTTCAAGTACTCAGACTACACGATGTGGACGGCC 2084

Db       1985 GCACACTGCTACATCGATGACAGAGGATTCAGGTACTCAGACCCCACGCAGTGGACGGCC 2044

Qy       2085 TTCCTGGGTCTGCTGGACCAGAGCAAGCGCAGTGCCTCTGGGGTGCAGGAGCTGAAGCTC 2144

Db       2045 TTCCTGGGCTTGCACGACCAGAGCCAGCGCAGCGCCCCTGGGGTGCAGGAGCGCAGGCTC 2104

Qy       2145 AAACGTATCATCACCCACCCTTCCTTCAATGATTTCACCTTCGACTATGACATCGCCTTG 2204

Db       2105 AAGCGCATCATCTCCCACCCCTTCTTCAATGACTTCACCTTCGACTATGACATCGCGCTG 2164

Qy       2205 CTGGAGCTGGAGAAGTCGGTGGAGTACAGCACCGTCGTGCGCCCCATCTGCCTGCCTGAT 2264

Db       2165 CTGGAGCTGGAGAAACCGGCAGAGTACAGCTCCATGGTGCGGCCCATCTGCCTGCCGGAC 2224

Qy       2265 GCTACCCATGTCTTCCCTGCTGGCAAGGCCATCTGGGTCACAGGCTGGGGGCACACAAAA 2324

Db       2225 GCCTCCCATGTCTTCCCTGCCGGCAAGGCCATCTGGGTCACGGGCTGGGGACACACCCAG 2284

Qy       2325 GAGGGAGGTACCGGAGCGCTGATCCTGCAGAAGGGTGAGATCCGTGTCATCAACCAGACC 2384

Db       2285 TATGGAGGCACTGGCGCGCTGATCCTGCAAAAGGGTGAGATCCGCGTCATCAACCAGACC 2344

Qy       2385 ACCTGTGAGGACCTCATGCCGCAGCAGATCACCCCACGAATGATGTGTGTGGGTTTCCTC 2444

Db       2345 ACCTGCGAGAACCTCCTGCCGCAGCAGATCACGCCGCGCATGATGTGCGTGGGCTTCCTC 2404

Qy       2445 AGTGGGGGTGTGGACTCCTGCCAGGGTGACTCTGGTGGCCCCTTGTCAAGCGCGGAGAAA 2504

Db       2405 AGCGGCGGCGTGGACTCCTGCCAGGGTGATTCCGGGGGACCCCTGTCCAGCGTGGAGGCG 2464

Qy       2505 GATGGGCGAATGTTCCAGGCTGGTGTGGTGAGCTGGGGTGAAGGCTGCGCTCAGAGGAAC 2564

Db       2465 GATGGGCGGATCTTCCAGGCCGGTGTGGTGAGCTGGGGAGACGGCTGCGCTCAGAGGAAC 2524

Qy       2565 AAGCCAGGCGTGTACACAAGGCTCCCTGTAGTTCGGGACTGGATCAAAGAGCACACTGGG 2624

Db       2525 AAGCCAGGCGTGTACACAAGGCTCCCTCTGTTTCGGGACTGGATCAAAGAGAACACTGGG 2584

Qy       2625 GTATAGCAGCATGGACAGACAGCCGACCACAAACACCCACAGGGATGCCCGACATGCACA 2684

Db       2585 GTATAGGGGCCGGG---GCCACCCAAATGTGTACACCTGCGGGGCCACCCATCGTCCACC 2641

Qy       2685 CCTGGATACAGGAGAGGAACACTGACGACATTTATGCTGTGGCCTCCCCCCCCCAACACA 2744

Db       2642 CCAGTGTGCACG-CCTGCAGGCTGGAGACTGGACCGCTGACTGCACCAGCGCCC-CCAGA 2699

Qy       2745 ACCCAGACTGTGAACTGCATCCTTAGGACTCAGAGT 2780

Db       2700 ACATACACTGTGAACTCAATCTCCAGGGCTCCAAAT 2735


RESULT 7
AAH23601
ID   AAH23601 standard; DNA; 3147 BP.
XX
AC   AAH23601;
XX
DT   03-AUG-2001  (first entry)
XX
DE   Human TADG-15 coding sequence.
XX
KW   Human; TADG-15; cytostatic; vaccine; ovarian tumour; cancer;
KW   tumour antigen-derived gene 15; extracellular serine protease; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             23..2590
FT                   /*tag=  a
FT                   /product= "Human TADG-15"
XX
PN   WO200129056-A1.
XX
PD   26-APR-2001.
XX
PF   20-OCT-2000; 2000WO-US29095.
XX
PR   20-OCT-1999;   99US-0421213.
XX
PA   (UYAR-) UNIV ARKANSAS.
XX
PI   O'Brien TJ,  Tanimoto H;
XX
DR   WPI; 2001-381031/40.
DR   P-PSDB; AAB98500.
XX
PT   Novel extracellular serine protease, termed tumor antigen-derived gene
PT   15 protein overexpressed in carcinomas and DNA encoding it, for
PT   diagnosis, treatment, prevention of cancer, particularly breast,
PT   ovarian cancer -
XX
PS   Claim 2; Fig 2; 130pp; English.
XX
CC   The present sequence is the coding sequence for human tumour
CC   antigen-derived gene 15 (TADG-15) protein. TADG-15 is an extracellular
CC   serine protease. It was found that TADG-15 is over-expressed in ovarian
CC   tumours. TADG-15 protein or its fragments of 9-20 residues that lack
CC   TADG-15 protease activity are useful for vaccinating an individual
CC   against TADG-15, having, suspected of having or at risk of getting
CC   cancer. Furthermore, the TADG-15 gene can be used as a diagnostic or
CC   therapeutic target in cancer.
XX
SQ   Sequence 3147 BP; 654 A; 952 C; 958 G; 583 T; 0 other;

  Query Match           60.6%;  Score 1883.2;  DB 22;  Length 3147;
  Best Local Similarity  81.2%;  Pred. No. 0;
  Matches 2223;  Conservative    0;  Mismatches  508;  Indels    5;  Gaps    3;

Qy         45 GATCGGACCGCCAAAACCATGGGTAGCAATCGGGGCCGCAAGGCCGGAGGGGGCTCTCAG 104

Db          5 GAGCGGCCTCGGGGTACCATGGGGAGCGATCGGGCCCGCAAGGGCGGAGGGGGCCCGAAG 64

Qy        105 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCTAGAGAACATGAATGGCTTTGAGGAG 164

Db         65 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCACGAGAAAGTGAATGGCTTGGAGGAA 124

Qy        165 GGTGTGGAGTTCCTGCCTGCGAACAATGCCAAGAAAGTGGAGAAGCGAGGCCCCAGGCGC 224

Db        125 GGCGTGGAGTTCCTGCCAGTCAACAACGTCAAGAAGGTGGAAAAGCATGGCCCGGGGCGC 184

Qy        225 TGGGTGGTGCTGGTGGCAGTGCTGTTCAGCTTCCTCTTGCTCTCCCTCATGGCTGGCTTG 284

Db        185 TGGGTGGTGCTGGCAGCCGTGCTGATCGGCCTCCTCTTGGTCTTGCTGGGGATCGGCTTC 244

Qy        285 CTGGTGTGGCACTTCCATTATCGGAATGTGCGGGTTCAAAAAGTCTTCAATGGCCATCTG 344

Db        245 CTGGTGTGGCATTTGCAGTACCGGGACGTGCGTGTCCAGAAGGTCTTCAATGGCTACATG 304

Qy        345 AGGATCACAAATGAGATCTTTCTGGATGCGTATGAGAACTCCACCTCCACAGAGTTTATC 404

Db        305 AGGATCACAAATGAGAATTTTGTGGATGCCTACGAGAACTCCAACTCCACTGAGTTTGTA 364

Qy        405 AGCCTGGCCAGCCAGGTGAAGGAGGCGCTGAAGCTGCTGTACAATGAAGTCCCTGTCCTG 464

Db        365 AGCCTGGCCAGCAAGGTGAAGGACGCGCTGAAGCTGCTGTACAGCGGAGTCCCATTCCTG 424

Qy        465 GGTCCCTACCACAAGAAGTCGGCTGTAACTGCCTTCAGTGAGGGCAGTGTCATCGCCTAC 524
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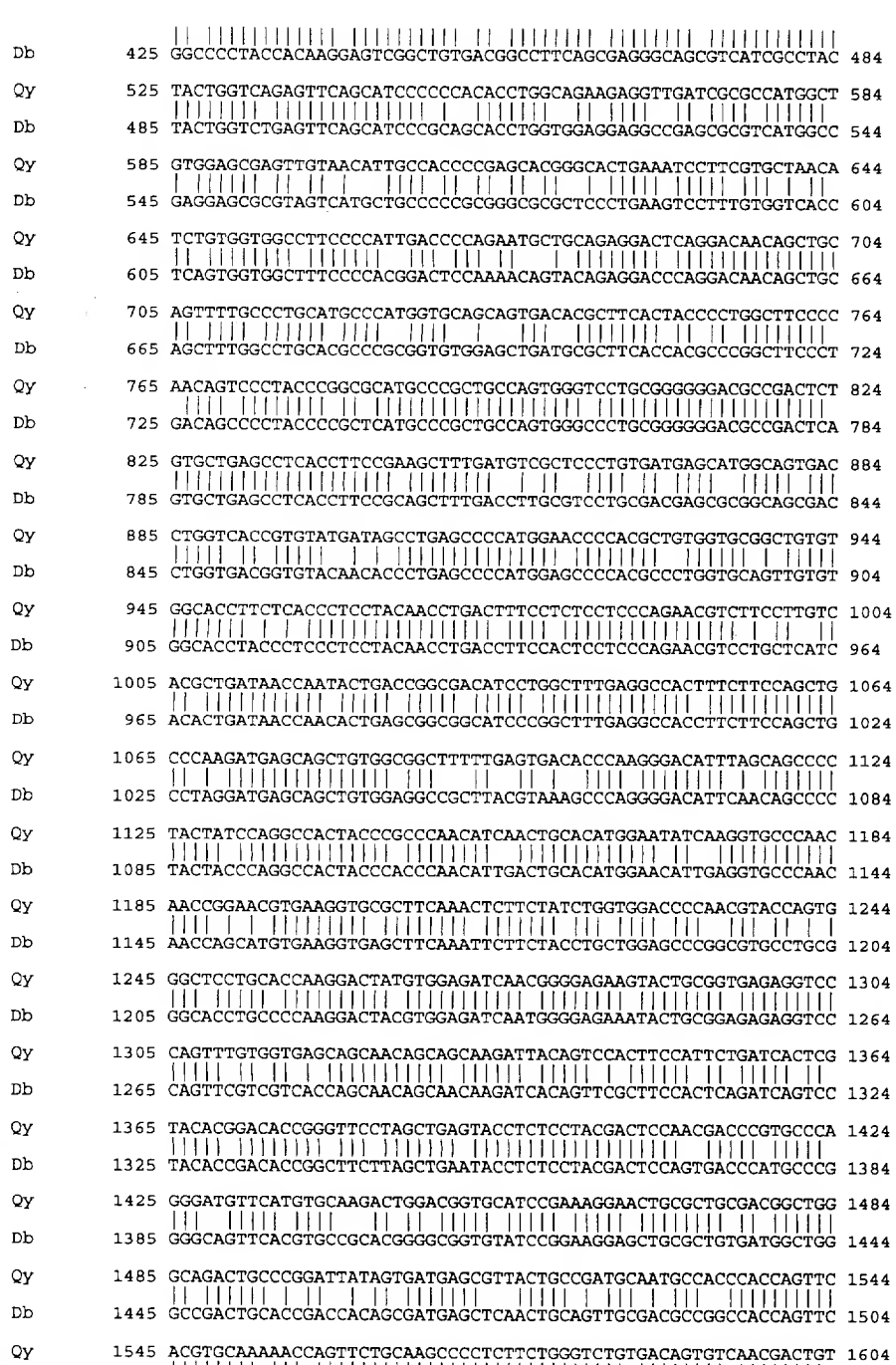

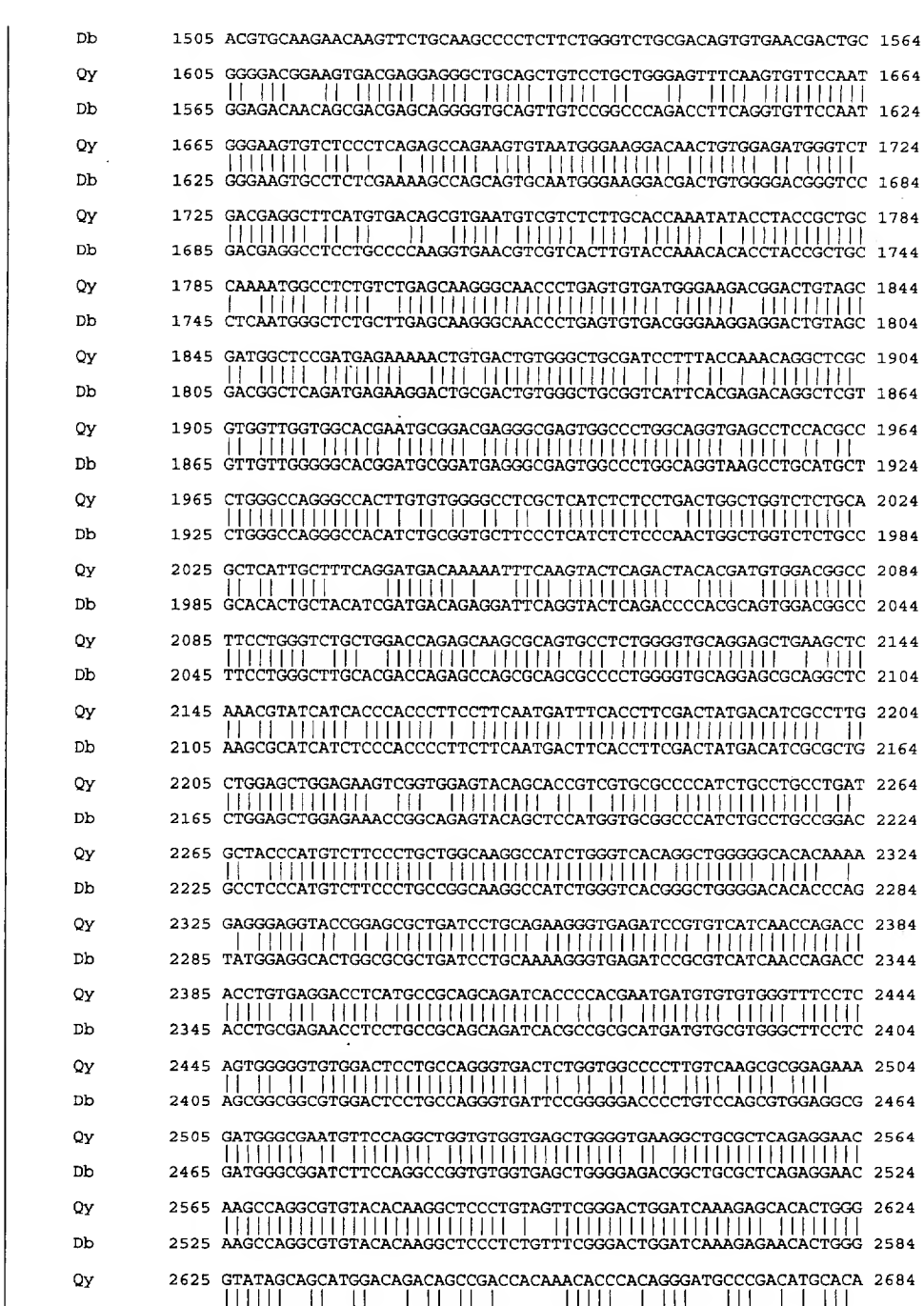

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Qy       2685 CCTGGATACAGGAGAGGAACACTGACGACATTTATGCTGTGGCCTCCCCCCCCCCAACACA 2744
Db       2642 CCAGTGTGCACG-CCTGCAGGCTGGAGACTGGACCGCTGACTGCACCAGCGCCC-CCAGA 2699

Qy       2745 ACCCAGACTGTGAACTGCATCCTTAGGACTCAGAGT 2780
Db       2700 ACATACACTGTGAACTCAATCTCCAGGGCTCCAAAT 2735
```

RESULT 8
AAH23609/c
ID AAH23609 standard; RNA; 3147 BP.
XX
AC AAH23609;
XX
DT 03-AUG-2001 (first entry)
XX
DE Human TADG-15 antisense RNA sequence.
XX
KW TADG-15; cytostatic; vaccine; ovarian tumour; cancer; human; antisense;
KW tumour antigen-derived gene 15; serine protease; ss.
XX
OS Homo sapiens.
XX
PN WO200129056-A1.
XX
PD 26-APR-2001.
XX
PF 20-OCT-2000; 2000WO-US29095.
XX
PR 20-OCT-1999; 99US-0421213.
XX
PA (UYAR-) UNIV ARKANSAS.
XX
PI O'Brien TJ, Tanimoto H;
XX
DR WPI; 2001-381031/40.
XX
PT Novel extracellular serine protease, termed tumor antigen-derived gene
PT 15 protein overexpressed in carcinomas and DNA encoding it, for
PT diagnosis, treatment, prevention of cancer, particularly breast,
PT ovarian cancer -
XX
PS Example 8; Page 102-103; 130pp; English.
XX
CC The present invention relates to human tumour antigen-derived gene 15
CC (TADG-15) protein and coding sequence (see AAH23601 and AAB98500).
CC TADG-15 is an extracellular serine protease. It was found that TADG-15 is
CC over-expressed in ovarian tumours. TADG-15 protein or its fragments of
CC 9-20 residues that lack TADG-15 protease activity are useful for
CC vaccinating an individual against TADG-15, having, suspected of having or
CC at risk of getting cancer. Furthermore, the TADG-15 gene can be used as a
CC diagnostic or therapeutic target in cancer. TADG-15 was cloned and
CC expressed in the opposite orientation such that an antisense RNA molecule
CC (the present sequence) was produced. The present sequence is useful for
CC hybridising to the complementary RNA in a cell and thereby inhibiting
CC translation of TADG-15 into protein.
XX
SQ Sequence 3147 BP; 583 A; 958 C; 952 G; 654 U; 0 other;

Query Match 60.6%; Score 1883.2; DB 22; Length 3147;
Best Local Similarity 81.2%; Pred. No. 0;
Matches 2223; Conservative 0; Mismatches 508; Indels 5; Gaps 3;

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Qy         45 GATCGGACCGCCAAAACCATGGGTAGCAATCGGGGCCGCAAGGCCGGAGGGGGCTCTCAG 104
Db       3143 GAGCGGCCTCGGGGTACCATGGGGAGCGATCGGGCCCGCAAGGGCGGAGGGGGCCCGAAG 3084

Qy        105 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCTAGAGAACATGAATGGCTTTGAGGAG 164
Db       3083 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCACGAGAAAGTGAATGGCTTGGAGGAA 3024

Qy        165 GGTGTGGAGTTCCTGCCTGCGAACAATGCCAAGAAAGTGGAGAAGCGAGGCCCCAGGCGC 224
Db       3023 GGCGTGGAGTTCCTGCCAGTCAACAACGTCAAGAAGGTGGAAAAGCATGGCCCGGGGCGC 2964

Qy        225 TGGGTGGTGCTGGTGGCAGTGCTGTTCAGCTTCCTCTTGCTCTCCCTCATGGCTGGCTTG 284
Db       2963 TGGGTGGTGCTGGCAGCCGTGCTGATCGGCCTCCTCTTGGTCTTGCTGGGGATCGGCTTC 2904

Qy        285 CTGGTGTGGCACTTCCATTATCGGAATGTGCGGGTTCAAAAAGTCTTCAATGGCCATCTG 344
Db       2903 CTGGTGTGGCATTTGCAGTACCGGGACGTGCGTGTCCAGAAGGTCTTCAATGGCTACATG 2844

Qy        345 AGGATCACAAATGAGATCTTTCTGGATGCGTATGAGAACTCCACCTCCACAGAGTTTATC 404
Db       2843 AGGATCACAAATGAGAATTTTGTGGATGCCTACGAGAACTCCAACTCCACTGAGTTTGTA 2784

Qy        405 AGCCTGGCCAGCCAGGTGAAGGAGGCGCTGAAGCTGCTGTACAATGAAGTCCCTGTCCTG 464
Db       2783 AGCCTGGCCAGCAAGGTGAAGGACGCGCTGAAGCTGCTGTACAGCGGAGTCCCATTCCTG 2724

Qy        465 GGTCCCTACCACAAGAAGTCGGCTGTAACTGCCTTCAGTGAGGGCAGTGTCATCGCCTAC 524
Db       2723 GGCCCCTACCACAAGGAGTCGGCTGTGACGGCCTTCAGCGAGGGCAGCGTCATCGCCTAC 2664

Qy        525 TACTGGTCAGAGTTCAGCATCCCCCCACACCTGGCAGAAGAGGTTGATCGCGCCATGGCT 584
Db       2663 TACTGGTCTGAGTTCAGCATCCCGCAGCACCTGGTGGAGGAGGCCGAGCGCGTCATGGCC 2604

Qy        585 GTGGAGCGAGTTGTAACATTGCCACCCCGAGCACGGGCACTGAAATCCTTCGTGCTAACA 644
Db       2603 GAGGAGCGCGTAGTCATGCTGCCCCCGCGGGCGCGCTCCCTGAAGTCCTTTGTGGTCACC 2544

Qy        645 TCTGTGGTGGCCTTCCCCATTGACCCCAGAATGCTGCAGAGGACTCAGGACAACAGCTGC 704
Db       2543 TCAGTGGTGGCTTTCCCCACGGACTCCAAAACAGTACAGAGGACCCAGGACAACAGCTGC 2484

Qy        705 AGTTTTGCCCTGCATGCCCATGGTGCAGCAGTGACACGCTTCACTACCCCTGGCTTCCCC 764
Db       2483 AGCTTTGGCCTGCACGCCCGCGGTGTGGAGCTGATGCGCTTCACCACGCCCGGCTTCCCT 2424

Qy        765 AACAGTCCCTACCCGGCGCATGCCCGCTGCCAGTGGGTCCTGCGGGGGGACGCCGACTCT 824
Db       2423 GACAGCCCCTACCCCGCTCATGCCCGCTGCCAGTGGGCCCTGCGGGGGGACGCCGACTCA 2364

Qy        825 GTGCTGAGCCTCACCTTCCGAAGCTTTGATGTCGCTCCCTGTGATGAGCATGGCAGTGAC 884
Db       2363 GTGCTGAGCCTCACCTTCCGCAGCTTTGACCTTGCGTCCTGCGACGAGCGCGGCAGCGAC 2304

Qy        885 CTGGTCACCGTGTATGATAGCCTGAGCCCCATGGAACCCCACGCTGTGGTGCGGCTGTGT 944
Db       2303 CTGGTGACGGTGTACAACACCCTGAGCCCCATGGAGCCCCACGCCCTGGTGCAGTTGTGT 2244

Qy        945 GGCACCTTCTCACCCTCCTACAACCTGACTTTCCTCTCCTCCCAGAACGTCTTCCTTGTC 1004
Db       2243 GGCACCTACCCTCCCTCCTACAACCTGACCTTCCACTCCTCCCAGAACGTCCTGCTCATC 2184

Qy       1005 ACGCTGATAACCAATACTGACCGGCGACATCCTGGCTTTGAGGCCACTTTCTTCCAGCTG 1064
Db       2183 ACACTGATAACCAACACTGAGCGGCGGCATCCCGGCTTTGAGGCCACCTTCTTCCAGCTG 2124

Qy       1065 CCCAAGATGAGCAGCTGTGGCGGCTTTTTGAGTGACACCCAAGGGACATTTAGCAGCCCC 1124
Db       2123 CCTAGGATGAGCAGCTGTGGAGGCCGCTTACGTAAAGCCCAGGGGACATTCAACAGCCCC 2064

Qy       1125 TACTATCCAGGCCACTACCCGCCCAACATCAACTGCACATGGAATATCAAGGTGCCCAAC 1184
Db       2063 TACTACCCAGGCCACTACCCACCCAACATTGACTGCACATGGAACATTGAGGTGCCCAAC 2004

Qy       1185 AACCGGAACGTGAAGGTGCGCTTCAAACTCTTCTATCTGGTGGACCCCAACGTACCAGTG 1244
Db       2003 AACCAGCATGTGAAGGTGAGCTTCAAATTCTTCTACCTGCTGGAGCCCGGCGTGCCTGCG 1944

Qy       1245 GGCTCCTGCACCAAGGACTATGTGGAGATCAACGGGGAGAAGTACTGCGGTGAGAGGTCC 1304
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Db       1943 GGCACCTGCCCCAAGGACTACGTGGAGATCAATGGGGAGAAATACTGCGGAGAGAGGTCC 1884
Qy       1305 CAGTTTGTGGTGAGCAGCAACAGCAGCAAGATTACAGTCCACTTCCATTCTGATCACTCG 1364
Db       1883 CAGTTCGTCGTCACCAGCAACAGCAACAAGATCACAGTTCGCTTCCACTCAGATCAGTCC 1824
Qy       1365 TACACGGACACCGGGTTCCTAGCTGAGTACCTCTCCTACGACTCCAACGACCCGTGCCCA 1424
Db       1823 TACACCGACACCGGCTTCTTAGCTGAATACCTCTCCTACGACTCCAGTGACCCATGCCCG 1764
Qy       1425 GGGATGTTCATGTGCAAGACTGGACGGTGCATCCGAAAGGAACTGCGCTGCGACGGCTGG 1484
Db       1763 GGGCAGTTCACGTGCCGCACGGGGCGGTGTATCCGGAAGGAGCTGCGCTGTGATGGCTGG 1704
Qy       1485 GCAGACTGCCCGGATTATAGTGATGAGCGTTACTGCCGATGCAATGCCACCCACCAGTTC 1544
Db       1703 GCCGACTGCACCGACCACAGCGATGAGCTCAACTGCAGTTGCGACGCCGGCCACCAGTTC 1644
Qy       1545 ACGTGCAAAAACCAGTTCTGCAAGCCCCTCTTCTGGGTCTGTGACAGTGTCAACGACTGT 1604
Db       1643 ACGTGCAAGAACAAGTTCTGCAAGCCCCTCTTCTGGGTCTGCGACAGTGTGAACGACTGC 1584
Qy       1605 GGGGACGGAAGTGACGAGGAGGGCTGCAGCTGTCCTGCTGGGAGTTTCAAGTGTTCCAAT 1664
Db       1583 GGAGACAACAGCGACGAGCAGGGGTGCAGTTGTCCGGCCCAGACCTTCAGGTGTTCCAAT 1524
Qy       1665 GGGAAGTGTCTCCCTCAGAGCCAGAAGTGTAATGGGAAGGACAACTGTGGAGATGGGTCT 1724
Db       1523 GGGAAGTGCCTCTCGAAAAGCCAGCAGTGCAATGGGAAGGACGACTGTGGGGACGGGTCC 1464
Qy       1725 GACGAGGCTTCATGTGACAGCGTGAATGTCGTCTCTTGCACCAAATATACCTACCGCTGC 1784
Db       1463 GACGAGGCCTCCTGCCCCAAGGTGAACGTCGTCACTTGTACCAAACACACCTACCGCTGC 1404
Qy       1785 CAAAATGGCCTCTGTCTGAGCAAGGGCAACCCTGAGTGTGATGGGAAGACGGACTGTAGC 1844
Db       1403 CTCAATGGGCTCTGCTTGAGCAAGGGCAACCCTGAGTGTGACGGGAAGGAGGACTGTAGC 1344
Qy       1845 GATGGCTCCGATGAGAAAAACTGTGACTGTGGGCTGCGATCCTTTACCAAACAGGCTCGC 1904
Db       1343 GACGGCTCAGATGAGAAGGACTGCGACTGTGGGCTGCGGTCATTCACGAGACAGGCTCGT 1284
Qy       1905 GTGGTTGGTGGCACGAATGCGGACGAGGGCGAGTGGCCCTGGCAGGTGAGCCTCCACGCC 1964
Db       1283 GTTGTTGGGGGCACGGATGCGGATGAGGGCGAGTGGCCCTGGCAGGTAAGCCTGCATGCT 1224
Qy       1965 CTGGGCCAGGGCCACTTGTGTGGGGCCTCGCTCATCTCTCCTGACTGGCTGGTCTCTGCA 2024
Db       1223 CTGGGCCAGGGCCACATCTGCGGTGCTTCCCTCATCTCTCCCAACTGGCTGGTCTCTGCC 1164
Qy       2025 GCTCATTGCTTTCAGGATGACAAAAATTTCAAGTACTCAGACTACACGATGTGGACGGCC 2084
Db       1163 GCACACTGCTACATCGATGACAGAGGATTCAGGTACTCAGACCCCACGCAGTGGACGGCC 1104
Qy       2085 TTCCTGGGTCTGCTGGACCAGAGCAAGCGCAGTGCCTCTGGGGTGCAGGAGCTGAAGCTC 2144
Db       1103 TTCCTGGGCTTGCACGACCAGAGCCAGCGCAGCGCCCCTGGGGTGCAGGAGCGCAGGCTC 1044
Qy       2145 AAACGTATCATCACCCACCCTTCCTTCAATGATTTCACCTTCGACTATGACATCGCCTTG 2204
Db       1043 AAGCGCATCATCTCCCACCCCTTCTTCAATGACTTCACCTTCGACTATGACATCGCGCTG 984
Qy       2205 CTGGAGCTGGAGAAGTCGGTGGAGTACAGCACCGTCGTGCGCCCCATCTGCCTGCCTGAT 2264
Db        983 CTGGAGCTGGAGAAACCGGCAGAGTACAGCTCCATGGTGCGGCCCATCTGCCTGCCGGAC 924
Qy       2265 GCTACCCATGTCTTCCCTGCTGGCAAGGCCATCTGGGTCACAGGCTGGGGGCACACAAAA 2324
Db        923 GCCTCCCATGTCTTCCCTGCCGGCAAGGCCATCTGGGTCACGGGCTGGGGACACACCCAG 864
Qy       2325 GAGGGAGGTACCGGAGCGCTGATCCTGCAGAAGGGTGAGATCCGTGTCATCAACCAGACC 2384
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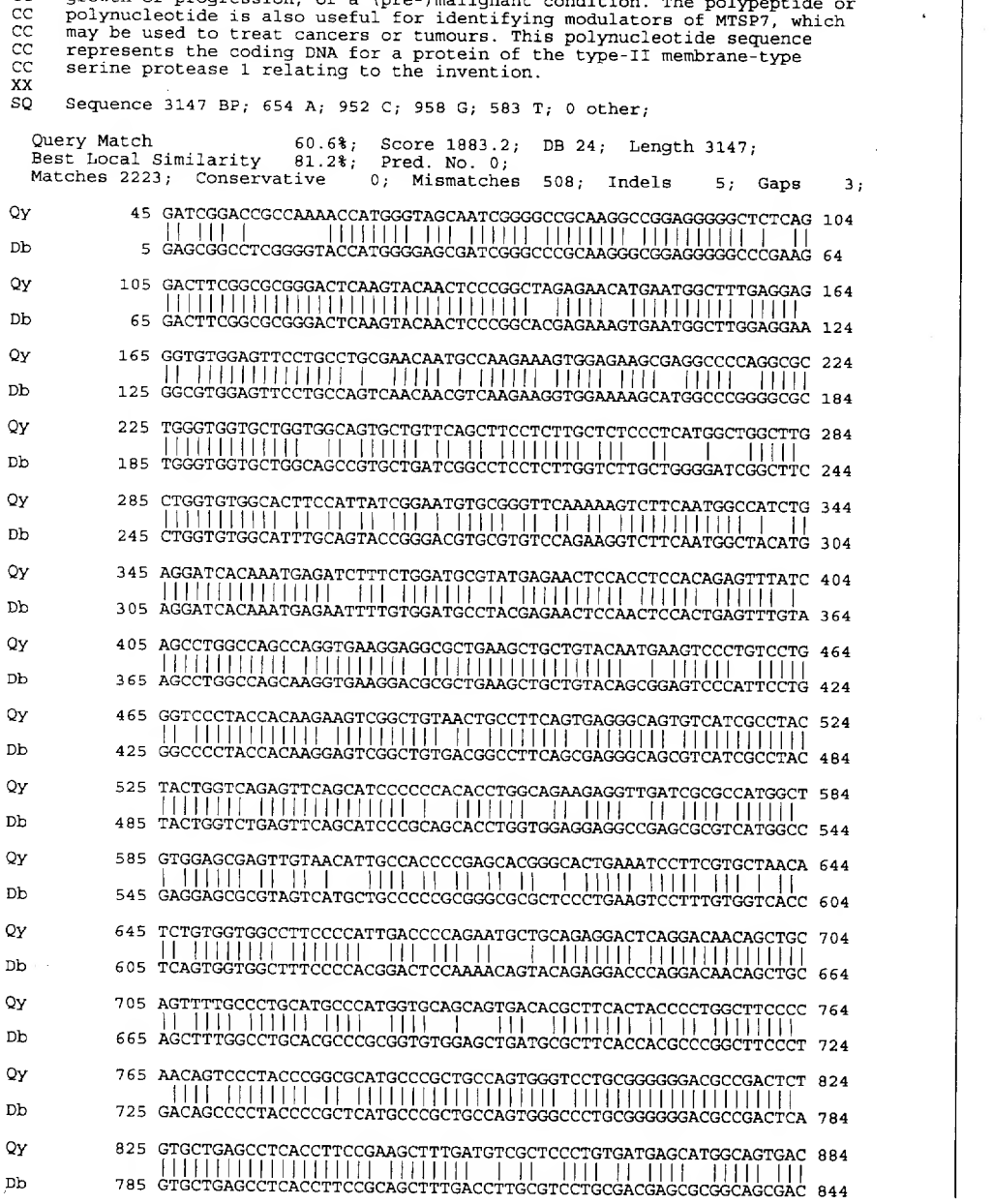
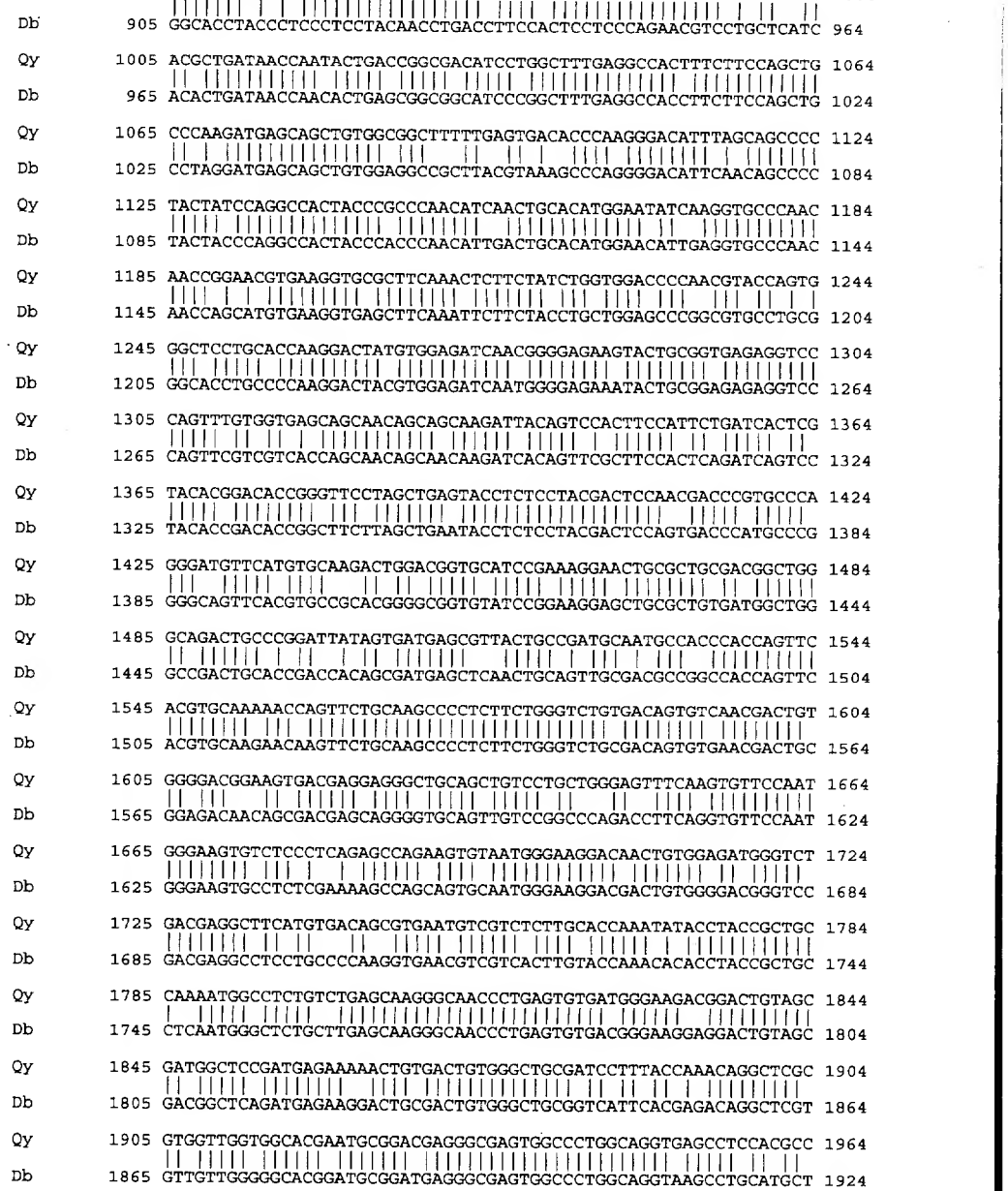
Db        863 TATGGAGGCACTGGCGCGCTGATCCTGCAAAAGGGTGAGATCCGCGTCATCAACCAGACC 804
Qy       2385 ACCTGTGAGGACCTCATGCCGCAGCAGATCACCCCACGAATGATGTGTGTGGGTTTCCTC 2444
Db        803 ACCTGCGAGAACCTCCTGCCGCAGCAGATCACGCCGCGCATGATGTGCGTGGGCTTCCTC 744
Qy       2445 AGTGGGGGTGTGGACTCCTGCCAGGGTGACTCTGGTGGCCCCTTGTCAAGCGCGGAGAAA 2504
Db        743 AGCGGCGGCGTGGACTCCTGCCAGGGTGATTCCGGGGGACCCCTGTCCAGCGTGGAGGCG 684
Qy       2505 GATGGGCGAATGTTCCAGGCTGGTGTGGTGAGCTGGGGTGAAGGCTGCGCTCAGAGGAAC 2564
Db        683 GATGGGCGGATCTTCCAGGCCGGTGTGGTGAGCTGGGGAGACGGCTGCGCTCAGAGGAAC 624
Qy       2565 AAGCCAGGCGTGTACACAAGGCTCCCTGTAGTTCGGGACTGGATCAAAGAGCACACTGGG 2624
Db        623 AAGCCAGGCGTGTACACAAGGCTCCCTCTGTTTCGGGACTGGATCAAAGAGAACACTGGG 564
Qy       2625 GTATAGCAGCATGGACAGACAGCCGACCACAAACACCCACAGGGATGCCCGACATGCACA 2684
Db        563 GTATAGGGGCCGGG---GCCACCCAAATGTGTACACCTGCGGGGCCACCCATCGTCCACC 507
Qy       2685 CCTGGATACAGGAGAGGAACACTGACGACATTTATGCTGTGGCCTCCCCCCCCCAACACA 2744
Db        506 CCAGTGTGCACG-CCTGCAGGCTGGAGACTGGACCGCTGACTGCACCAGCGCCC-CCAGA 449
Qy       2745 ACCCAGACTGTGAACTGCATCCTTAGGACTCAGAGT 2780
Db        448 ACATACACTGTGAACTCAATCTCCAGGGCTCCAAAT 413
```

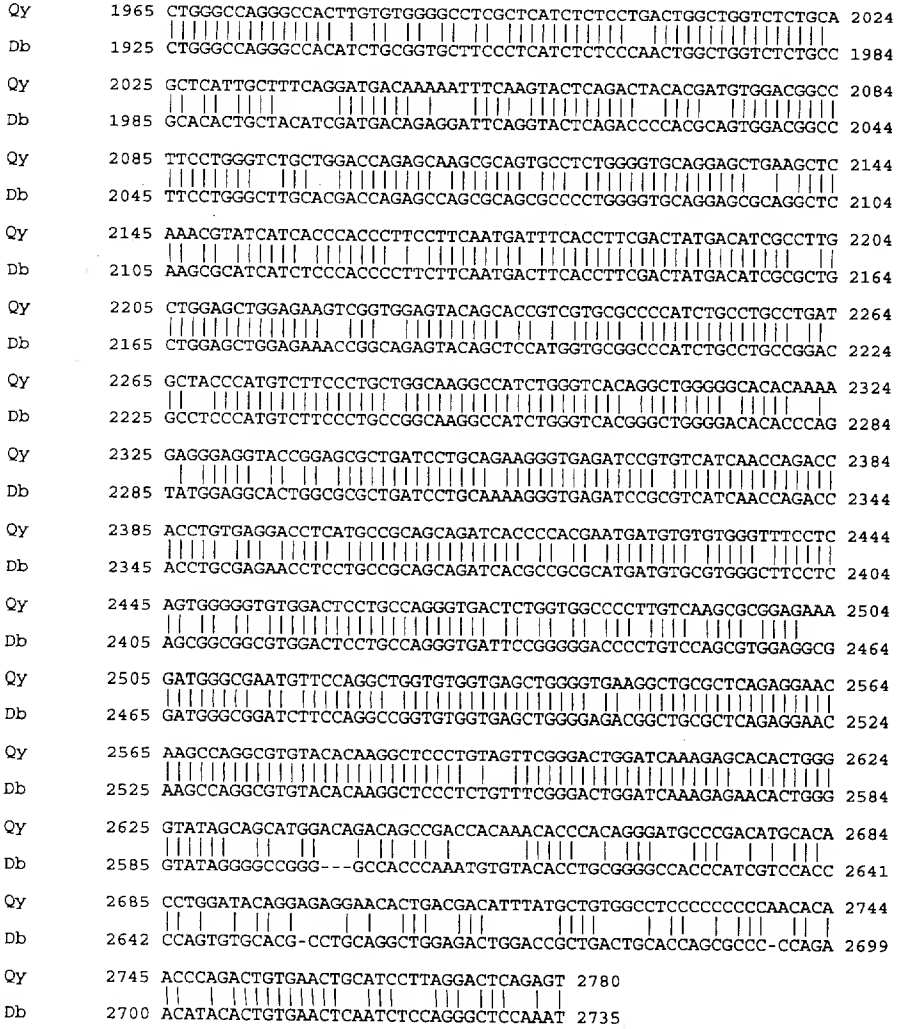
RESULT 9
AAL53444
ID   AAL53444 standard; DNA; 3147 BP.
XX
AC   AAL53444;
XX
DT   12-DEC-2002 (first entry)
XX
DE   Type II transmembrane serine protease 1 coding DNA SEQ ID No 1.
XX
KW   Cytostatic; type-II membrane-type serine protease 7; MTSP7; malignancy;
KW   neoplastic disease; pre-malignant lesion; tumour; zymogen form; cancer;
KW   malignant; enzyme; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200272786-A2.
XX
PD   19-SEP-2002.
XX
PF   13-MAR-2002; 2002WO-US07903.
XX
PR   13-MAR-2001; 2001US-275592P.
XX
PA   (CORV-) CORVAS INT INC.
XX
PI   Madison EL, Ong EO;
XX
DR   WPI; 2002-732827/79.
DR   P-PSDB; AAO22929.
XX
PT   New transmembrane serine protease 7 (MTSP7) polypeptide for diagnosing
PT   neoplastic diseases, monitoring tumor progress or therapeutic
PT   effectiveness, or identifying MTSP7 modulators for treating tumors or
PT   cancers -
XX
PS   Disclosure; Page 168-172; 184pp; English.
XX
CC   The invention relates to a purified single or two-chain polypeptide,
CC   which comprises the protease domain of a type-II membrane-type serine
CC   protease 7 (MTSP7) or its catalytically active portion. The polypeptide
CC   comprising MTSP7 is useful for detecting or diagnosing a neoplastic

CC disease, a pre-malignant lesion, a malignancy or other pathologic
CC condition in a subject. This polypeptide is also useful for monitoring
CC tumour (e.g. tumuor of the breast, cervix, prostate, lung, ovary or
CC colon) progress and/or therapeutic effectiveness. The inhibitor of the
CC polypeptide or the inhibitor of the polypeptide's zymogen form is useful
CC for treating or preventing a neoplastic disease, or tumour initiation,
CC growth or progression, or a (pre-)malignant condition. The polypeptide or
CC polynucleotide is also useful for identifying modulators of MTSP7, which
CC may be used to treat cancers or tumours. This polynucleotide sequence
CC represents the coding DNA for a protein of the type-II membrane-type
CC serine protease 1 relating to the invention.
XX
SQ Sequence 3147 BP; 654 A; 952 C; 958 G; 583 T; 0 other;

Query Match 60.6%; Score 1883.2; DB 24; Length 3147;
Best Local Similarity 81.2%; Pred. No. 0;
Matches 2223; Conservative 0; Mismatches 508; Indels 5; Gaps 3;



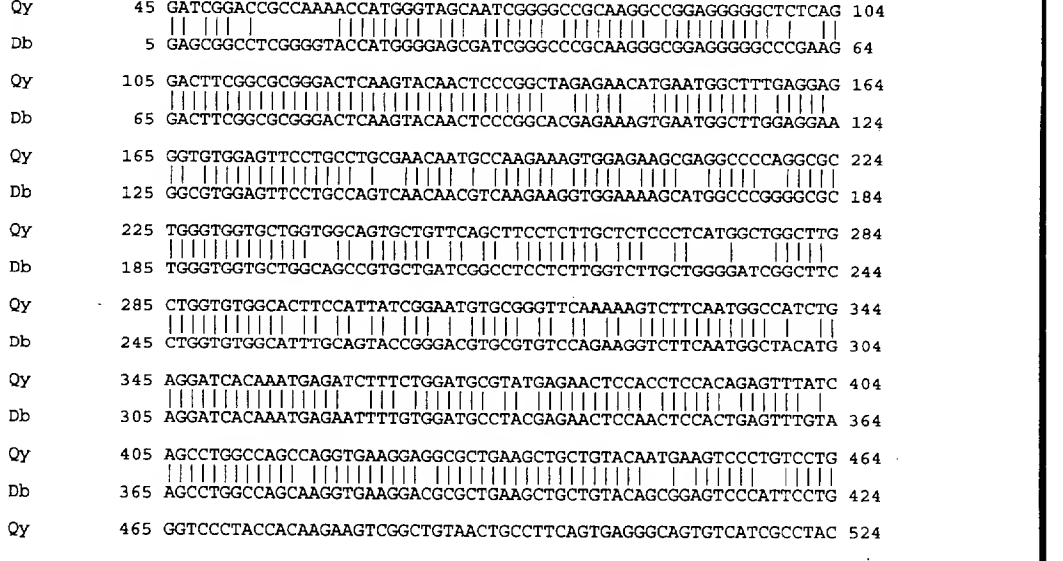


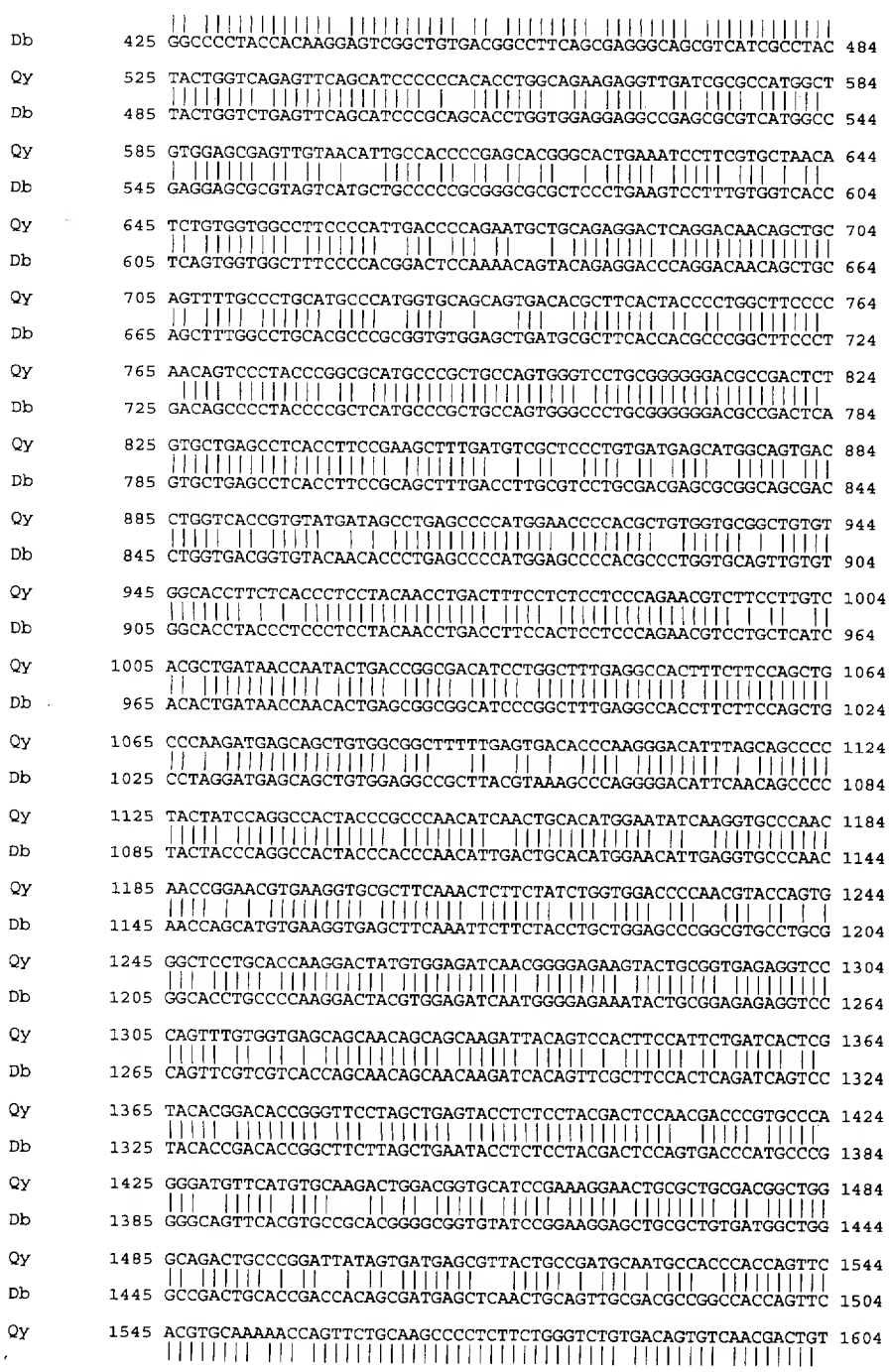


RESULT 10
AAL53445
ID AAL53445 standard; DNA; 3147 BP.
XX
AC AAL53445;
XX
DT 12-DEC-2002 (first entry)
XX
DE Type II transmembrane serine protease 1 domain DNA SEQ ID No 3.
XX
KW Cytostatic; type-II membrane-type serine protease 7; MTSP7; malignancy;
KW neoplastic disease; pre-malignant lesion; tumour; zymogen form; cancer;
KW malignant; enzyme; gene; ds.
XX
OS Homo sapiens.
XX

PN WO200272786-A2.
XX
PD 19-SEP-2002.
XX
PF 13-MAR-2002; 2002WO-US07903.
XX
PR 13-MAR-2001; 2001US-275592P.
XX
PA (CORV-) CORVAS INT INC.
XX
PI Madison EL, Ong EO;
XX
DR WPI; 2002-732827/79.
DR P-PSDB; AAO22930.
XX
PT New transmembrane serine protease 7 (MTSP7) polypeptide for diagnosing
PT neoplastic diseases, monitoring tumor progress or therapeutic
PT effectiveness, or identifying MTSP7 modulators for treating tumors or
PT cancers -
XX
PS Disclosure; Page 174-176; 184pp; English.
XX
CC The invention relates to a purified single or two-chain polypeptide,
CC which comprises the protease domain of a type-II membrane-type serine
CC protease 7 (MTSP7) or its catalytically active portion. The polypeptide
CC comprising MTSP7 is useful for detecting or diagnosing a neoplastic
CC disease, a pre-malignant lesion, a malignancy or other pathologic
CC condition in a subject. This polypeptide is also useful for monitoring
CC tumour (e.g. tumuor of the breast, cervix, prostate, lung, ovary or
CC colon) progress and/or therapeutic effectiveness. The inhibitor of the
CC polypeptide or the inhibitor of the polypeptide's zymogen form is useful
CC for treating or preventing a neoplastic disease, or tumour initiation,
CC growth or progression, or a (pre-)malignant condition. The polypeptide or
CC polynucleotide is also useful for identifying modulators of MTSP7, which
CC may be used to treat cancers or tumours. This polynucleotide sequence
CC represents the coding DNA for a protein domain of the type-II membrane-
CC type serine protease 1 relating to the invention.
XX
SQ Sequence 3147 BP; 654 A; 952 C; 958 G; 583 T; 0 other;

Query Match 60.6%; Score 1883.2; DB 24; Length 3147;
Best Local Similarity 81.2%; Pred. No. 0;
Matches 2223; Conservative 0; Mismatches 508; Indels 5; Gaps 3;

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Qy 525 TACTGGTCAGAGTTCAGCATCCCCCCACACCTGGCAGAAGAGGTTGATCGCGCCATGGCT 584
Db 485 TACTGGTCTGAGTTCAGCATCCCGCAGCACCTGGTGGAGGAGGCCGAGCGCGTCATGGCC 544
Qy 585 GTGGAGCGAGTTGTAACATTGCCACCCCGAGCACGGGCACTGAAATCCTTCGTGCTAACA 644
Db 545 GAGGAGCGCGTAGTCATGCTGCCCCCGCGGGCGCGCTCCCTGAAGTCCTTTGTGGTCACC 604
Qy 645 TCTGTGGTGGCCTTCCCCATTGACCCCAGAATGCTGCAGAGGACTCAGGACAACAGCTGC 704
Db 605 TCAGTGGTGGCTTTCCCCACGGACTCCAAAACAGTACAGAGGACCCAGGACAACAGCTGC 664
Qy 705 AGTTTTGCCCTGCATGCCCATGGTGCAGCAGTGACACGCTTCACTACCCCTGGCTTCCCC 764
Db 665 AGCTTTGGCCTGCACGCCCGCGGTGTGGAGCTGATGCGCTTCACCACGCCCGGCTTCCCT 724
Qy 765 AACAGTCCCTACCCGGCGCATGCCCGCTGCCAGTGGGTCCTGCGGGGGGACGCCGACTCT 824
Db 725 GACAGCCCCTACCCCGCTCATGCCCGCTGCCAGTGGGCCCTGCGGGGGGACGCCGACTCA 784
Qy 825 GTGCTGAGCCTCACCTTCCGAAGCTTTGATGTCGCTCCCTGTGATGAGCATGGCAGTGAC 884
Db 785 GTGCTGAGCCTCACCTTCCGCAGCTTTGACCTTGCGTCCTGCGACGAGCGCGGCAGCGAC 844
Qy 885 CTGGTCACCGTGTATGATAGCCTGAGCCCCATGGAACCCCACGCTGTGGTGCGGCTGTGT 944
Db 845 CTGGTGACGGTGTACAACACCCTGAGCCCCATGGAGCCCCACGCCCTGGTGCAGTTGTGT 904
Qy 945 GGCACCTTCTCACCCTCCTACAACCTGACTTTCCTCTCCTCCCAGAACGTCTTCCTTGTC 1004
Db 905 GGCACCTACCCTCCCTCCTACAACCTGACCTTCCACTCCTCCCAGAACGTCCTGCTCATC 964
Qy 1005 ACGCTGATAACCAATACTGACCGGCGACATCCTGGCTTTGAGGCCACTTTCTTCCAGCTG 1064
Db 965 ACACTGATAACCAACACTGAGCGGCGGCATCCCGGCTTTGAGGCCACCTTCTTCCAGCTG 1024
Qy 1065 CCCAAGATGAGCAGCTGTGGCGGCTTTTTGAGTGACACCCAAGGGACATTTAGCAGCCCC 1124
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Qy 1125 TACTATCCAGGCCACTACCCGCCCAACATCAACTGCACATGGAATATCAAGGTGCCCAAC 1184
Db 1085 TACTACCCAGGCCACTACCCACCCAACATTGACTGCACATGGAACATTGAGGTGCCCAAC 1144
Qy 1185 AACCGGAACGTGAAGGTGCGCTTCAAACTCTTCTATCTGGTGGACCCCAACGTACCAGTG 1244
Db 1145 AACCAGCATGTGAAGGTGAGCTTCAAATTCTTCTACCTGCTGGAGCCCGGCGTGCCTGCG 1204
Qy 1245 GGCTCCTGCACCAAGGACTATGTGGAGATCAACGGGGAGAAGTACTGCGGTGAGAGGTCC 1304
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Db 1265 CAGTTCGTCGTCACCAGCAACAGCAACAAGATCACAGTTCGCTTCCACTCAGATCAGTCC 1324
Qy 1365 TACACGGACACCGGGTTCCTAGCTGAGTACCTCTCCTACGACTCCAACGACCCGTGCCCA 1424
Db 1325 TACACCGACACCGGCTTCTTAGCTGAATACCTCTCCTACGACTCCAGTGACCCATGCCCG 1384
Qy 1425 GGGATGTTCATGTGCAAGACTGGACGGTGCATCCGAAAGGAACTGCGCTGCGACGGCTGG 1484
Db 1385 GGGCAGTTCACGTGCCGCACGGGGCGGTGTATCCGGAAGGAGCTGCGCTGTGATGGCTGG 1444
Qy 1485 GCAGACTGCCCGGATTATAGTGATGAGCGTTACTGCCGATGCAATGCCACCCACCAGTTC 1544
Db 1445 GCCGACTGCACCGACCACAGCGATGAGCTCAACTGCAGTTGCGACGCCGGCCACCAGTTC 1504
Qy 1545 ACGTGCAAAAACCAGTTCTGCAAGCCCCTCTTCTGGGTCTGTGACAGTGTCAACGACTGT 1604
Db 1505 ACGTGCAAGAACAAGTTCTGCAAGCCCCTCTTCTGGGTCTGCGACAGTGTGAACGACTGC 1564
Qy 1605 GGGGACGGAAGTGACGAGGAGGGCTGCAGCTGTCCTGCTGGGAGTTTCAAGTGTTCCAAT 1664
Db 1565 GGAGACAACAGCGACGAGCAGGGGTGCAGTTGTCCGGCCCAGACCTTCAGGTGTTCCAAT 1624
Qy 1665 GGGAAGTGTCTCCCTCAGAGCCAGAAGTGTAATGGGAAGGACAACTGTGGAGATGGGTCT 1724
Db 1625 GGGAAGTGCCTCTCGAAAAGCCAGCAGTGCAATGGGAAGGACGACTGTGGGGACGGGTCC 1684
Qy 1725 GACGAGGCTTCATGTGACAGCGTGAATGTCGTCTCTTGCACCAAATATACCTACCGCTGC 1784
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Qy 1785 CAAAATGGCCTCTGTCTGAGCAAGGGCAACCCTGAGTGTGATGGGAAGACGGACTGTAGC 1844
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Db 1805 GACGGCTCAGATGAGAAGGACTGCGACTGTGGGCTGCGGTCATTCACGAGACAGGCTCGT 1864
Qy 1905 GTGGTTGGTGGCACGAATGCGGACGAGGGCGAGTGGCCCTGGCAGGTGAGCCTCCACGCC 1964
Db 1865 GTTGTTGGGGGCACGGATGCGGATGAGGGCGAGTGGCCCTGGCAGGTAAGCCTGCATGCT 1924
Qy 1965 CTGGGCCAGGGCCACTTGTGTGGGGCCTCGCTCATCTCTCCTGACTGGCTGGTCTCTGCA 2024
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Db 2045 TTCCTGGGCTTGCACGACCAGAGCCAGCGCAGCGCCCCTGGGGTGCAGGAGCGCAGGCTC 2104
Qy 2145 AAACGTATCATCACCCACCCTTCCTTCAATGATTTCACCTTCGACTATGACATCGCCTTG 2204
Db 2105 AAGCGCATCATCTCCCACCCCTTCTTCAATGACTTCACCTTCGACTATGACATCGCGCTG 2164
Qy 2205 CTGGAGCTGGAGAAGTCGGTGGAGTACAGCACCGTCGTGCGCCCCATCTGCCTGCCTGAT 2264
Db 2165 CTGGAGCTGGAGAAACCGGCAGAGTACAGCTCCATGGTGCGGCCCATCTGCCTGCCGGAC 2224
Qy 2265 GCTACCCATGTCTTCCCTGCTGGCAAGGCCATCTGGGTCACAGGCTGGGGGCACACAAAA 2324
Db 2225 GCCTCCCATGTCTTCCCTGCCGGCAAGGCCATCTGGGTCACGGGCTGGGGACACACCCAG 2284
Qy 2325 GAGGGAGGTACCGGAGCGCTGATCCTGCAGAAGGGTGAGATCCGTGTCATCAACCAGACC 2384
Db 2285 TATGGAGGCACTGGCGCGCTGATCCTGCAAAAGGGTGAGATCCGCGTCATCAACCAGACC 2344
Qy 2385 ACCTGTGAGGACCTCATGCCGCAGCAGATCACCCCACGAATGATGTGTGTGGGTTTCCTC 2444
Db 2345 ACCTGCGAGAACCTCCTGCCGCAGCAGATCACGCCGCGCATGATGTGCGTGGGCTTCCTC 2404
Qy 2445 AGTGGGGGTGTGGACTCCTGCCAGGGTGACTCTGGTGGCCCCTTGTCAAGCGCGGAGAAA 2504
Db 2405 AGCGGCGGCGTGGACTCCTGCCAGGGTGATTCCGGGGGACCCCTGTCCAGCGTGGAGGCG 2464
Qy 2505 GATGGGCGAATGTTCCAGGCTGGTGTGGTGAGCTGGGGTGAAGGCTGCGCTCAGAGGAAC 2564
Db 2465 GATGGGCGGATCTTCCAGGCCGGTGTGGTGAGCTGGGGAGACGGCTGCGCTCAGAGGAAC 2524
Qy 2565 AAGCCAGGCGTGTACACAAGGCTCCCTGTAGTTCGGGACTGGATCAAAGAGCACACTGGG 2624
Db 2525 AAGCCAGGCGTGTACACAAGGCTCCCTCTGTTTCGGGACTGGATCAAAGAGAACACTGGG 2584
Qy 2625 GTATAGCAGCATGGACAGACAGCCGACCACAAACACCCACAGGGATGCCCGACATGCACA 2684
Db 2585 GTATAGGGGCCGGG---GCCACCCAAATGTGTACACCTGCGGGGCCACCCATCGTCCACC 2641

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Qy       2685 CCTGGATACAGGAGAGGAACACTGACGACATTTATGCTGTGGCCTCCCCCCCCCAACACA 2744
Db       2642 CCAGTGTGCACG-CCTGCAGGCTGGAGACTGGACCGCTGACTGCACCAGCGCCC-CCAGA 2699

Qy       2745 ACCCAGACTGTGAACTGCATCCTTAGGACTCAGAGT 2780
Db       2700 ACATACACTGTGAACTCAATCTCCAGGGCTCCAAAT 2735


RESULT 11
ABZ58500
ID   ABZ58500 standard; cDNA; 3147 BP.
XX
AC   ABZ58500;
XX
DT   13-MAY-2003  (first entry)
XX
DE   Transmembrane serine protease 1 (MTSP1) cDNA.
XX
KW   Human; transmembrane serine protease 1; MTSP1; MTSP20; enzyme;
KW   cytostatic; dermatological; cardiant; vulnerary; ophthalmological;
KW   gene therapy; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             23..2590
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XX
PN   WO2003004681-A2.
XX
PD   16-JAN-2003.
XX
PF   03-JUL-2002; 2002WO-US21208.
XX
PR   03-JUL-2001; 2001US-302939P.
XX
PA   (CORV-) CORVAS INT INC.
XX
PI   Madison EL,  Ong EO;
XX
DR   WPI; 2003-239207/23.
DR   P-PSDB; ABP72376.
XX
PT   New type-II membrane-type serine protease 20 polypeptides, useful for
PT   preparing a medicament for diagnosing, treating or preventing cancer,
PT   dermatological disorders, aberrant wound repairs or crest syndromes -
XX
PS   Disclosure; Page 194-198; 216pp; English.
XX
CC   The present sequence is that of cDNA encoding human type II
CC   transmembrane serine protease 1 (MTSP1).  The invention relates
CC   to novel human type II transmembrane serine protein 20 (MTSP20)
CC   (see ABP72374) and nucleic acids encoding it (see ABZ58499).
CC   Also claimed are methods of inhibiting tumour initiation, growth
CC   or progression by inhibiting MTSP20 activity, and of treating or
CC   preventing a disease or disorder associated with undesired and/or
CC   uncontrolled angiogenesis or neovascularisation, especially
CC   undesired angiogenesis associated with solid neoplasms, vascular
CC   malformations and cardiovascular disorders, chronic inflammatory
CC   diseases, aberrant wound repairs, circulatory disorders, crest
CC   syndromes, dermatological disorders and ocular disorders using
CC   an inhibitor of MTSP20.
XX
SQ   Sequence 3147 BP; 654 A; 952 C; 958 G; 583 T; 0 other;

  Query Match           60.6%;  Score 1883.2;  DB 25;  Length 3147;
  Best Local Similarity  81.2%;  Pred. No. 0;
  Matches 2223;  Conservative    0;  Mismatches  508;  Indels    5;  Gaps    3;

Qy         45 GATCGGACCGCCAAAACCATGGGTAGCAATCGGGGCCGCAAGGCCGGAGGGGGCTCTCAG 104

Db          5 GAGCGGCCTCGGGGTACCATGGGGAGCGATCGGGCCCGCAAGGGCGGAGGGGGCCCGAAG 64

Qy        105 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCTAGAGAACATGAATGGCTTTGAGGAG 164

Db         65 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCACGAGAAAGTGAATGGCTTGGAGGAA 124

Qy        165 GGTGTGGAGTTCCTGCCTGCGAACAATGCCAAGAAAGTGGAGAAGCGAGGCCCCAGGCGC 224

Db        125 GGCGTGGAGTTCCTGCCAGTCAACAACGTCAAGAAGGTGGAAAAGCATGGCCCGGGGCGC 184

Qy        225 TGGGTGGTGCTGGTGGCAGTGCTGTTCAGCTTCCTCTTGCTCTCCCTCATGGCTGGCTTG 284

Db        185 TGGGTGGTGCTGGCAGCCGTGCTGATCGGCCTCCTCTTGGTCTTGCTGGGGATCGGCTTC 244

Qy        285 CTGGTGTGGCACTTCCATTATCGGAATGTGCGGGTTCAAAAAGTCTTCAATGGCCATCTG 344

Db        245 CTGGTGTGGCATTTGCAGTACCGGGACGTGCGTGTCCAGAAGGTCTTCAATGGCTACATG 304

Qy        345 AGGATCACAAATGAGATCTTTCTGGATGCGTATGAGAACTCCACCTCCACAGAGTTTATC 404

Db        305 AGGATCACAAATGAGAATTTTGTGGATGCCTACGAGAACTCCAACTCCACTGAGTTTGTA 364

Qy        405 AGCCTGGCCAGCCAGGTGAAGGAGGCGCTGAAGCTGCTGTACAATGAAGTCCCTGTCCTG 464

Db        365 AGCCTGGCCAGCAAGGTGAAGGACGCGCTGAAGCTGCTGTACAGCGGAGTCCCATTCCTG 424

Qy        465 GGTCCCTACCACAAGAAGTCGGCTGTAACTGCCTTCAGTGAGGGCAGTGTCATCGCCTAC 524

Db        425 GGCCCCTACCACAAGGAGTCGGCTGTGACGGCCTTCAGCGAGGGCAGCGTCATCGCCTAC 484

Qy        525 TACTGGTCAGAGTTCAGCATCCCCCCACACCTGGCAGAAGAGGTTGATCGCGCCATGGCT 584

Db        485 TACTGGTCTGAGTTCAGCATCCCGCAGCACCTGGTGGAGGAGGCCGAGCGCGTCATGGCC 544

Qy        585 GTGGAGCGAGTTGTAACATTGCCACCCCGAGCACGGGCACTGAAATCCTTCGTGCTAACA 644

Db        545 GAGGAGCGCGTAGTCATGCTGCCCCCGCGGGCGCGCTCCCTGAAGTCCTTTGTGGTCACC 604

Qy        645 TCTGTGGTGGCCTTCCCCATTGACCCCAGAATGCTGCAGAGGACTCAGGACAACAGCTGC 704

Db        605 TCAGTGGTGGCTTTCCCCACGGACTCCAAAACAGTACAGAGGACCCAGGACAACAGCTGC 664

Qy        705 AGTTTTGCCCTGCATGCCCATGGTGCAGCAGTGACACGCTTCACTACCCCTGGCTTCCCC 764

Db        665 AGCTTTGGCCTGCACGCCCGCGGTGTGGAGCTGATGCGCTTCACCACGCCCGGCTTCCCT 724

Qy        765 AACAGTCCCTACCCGGCGCATGCCCGCTGCCAGTGGGTCCTGCGGGGGGGACGCCGACTCT 824

Db        725 GACAGCCCCTACCCCGCTCATGCCCGCTGCCAGTGGGCCCTGCGGGGGGACGCCGACTCA 784

Qy        825 GTGCTGAGCCTCACCTTCCGAAGCTTTGATGTCGCTCCCTGTGATGAGCATGGCAGTGAC 884

Db        785 GTGCTGAGCCTCACCTTCCGCAGCTTTGACCTTGCGTCCTGCGACGAGCGCGGCAGCGAC 844

Qy        885 CTGGTCACCGTGTATGATAGCCTGAGCCCCATGGAACCCCACGCTGTGGTGCGGCTGTGT 944

Db        845 CTGGTGACGGTGTACAACACCCTGAGCCCCATGGAGCCCCACGCCCTGGTGCAGTTGTGT 904

Qy        945 GGCACCTTCTCACCCTCCTACAACCTGACTTTCCTCTCCTCCCAGAACGTCTTCCTTGTC 1004

Db        905 GGCACCTACCCTCCCTCCTACAACCTGACCTTCCACTCCTCCCAGAACGTCCTGCTCATC 964

Qy       1005 ACGCTGATAACCAATACTGACCGGCGACATCCTGGCTTTGAGGCCACTTTCTTCCAGCTG 1064

Db        965 ACACTGATAACCAACACTGAGCGGCGGCATCCCGGCTTTGAGGCCACCTTCTTCCAGCTG 1024

Qy       1065 CCCAAGATGAGCAGCTGTGGCGGCTTTTTGAGTGACACCCAAGGGACATTTAGCAGCCCC 1124

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Qy       1125 TACTATCCAGGCCACTACCCGCCCAACATCAACTGCACATGGAATATCAAGGTGCCCAAC 1184
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Qy       1305 CAGTTTGTGGTGAGCAGCAACAGCAGCAAGATTACAGTCCACTTCCATTCTGATCACTCG 1364
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Qy       1425 GGGATGTTCATGTGCAAGACTGGACGGTGCATCCGAAAGGAACTGCGCTGCGACGGCTGG 1484
Db       1385 GGGCAGTTCACGTGCCGCACGGGGCGGTGTATCCGGAAGGAGCTGCGCTGTGATGGCTGG 1444
Qy       1485 GCAGACTGCCCGGATTATAGTGATGAGCGTTACTGCCGATGCAATGCCACCCACCAGTTC 1544
Db       1445 GCCGACTGCACCGACCACAGCGATGAGCTCAACTGCAGTTGCGACGCCGGCCACCAGTTC 1504
Qy       1545 ACGTGCAAAAACCAGTTCTGCAAGCCCCTCTTCTGGGTCTGTGACAGTGTCAACGACTGT 1604
Db       1505 ACGTGCAAGAACAAGTTCTGCAAGCCCCTCTTCTGGGTCTGCGACAGTGTGAACGACTGC 1564
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Db       1565 GGAGACAACAGCGACGAGCAGGGGTGCAGTTGTCCGGCCCAGACCTTCAGGTGTTCCAAT 1624
Qy       1665 GGGAAGTGTCTCCCTCAGAGCCAGAAGTGTAATGGGAAGGACAACTGTGGAGATGGGTCT 1724
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Qy       1725 GACGAGGCTTCATGTGACAGCGTGAATGTCGTCTCTTGCACCAAATATACCTACCGCTGC 1784
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Qy       1905 GTGGTTGGTGGCACGAATGCGGACGAGGGCGAGTGGCCCTGGCAGGTGAGCCTCCACGCC 1964
Db       1865 GTTGTTGGGGGCACGGATGCGGATGAGGGCGAGTGGCCCTGGCAGGTAAGCCTGCATGCT 1924
Qy       1965 CTGGGCCAGGGCCACTTGTGTGGGGCCTCGCTCATCTCTCCTGACTGGCTGGTCTCTGCA 2024
Db       1925 CTGGGCCAGGGCCACATCTGCGGTGCTTCCCTCATCTCTCCCAACTGGCTGGTCTCTGCC 1984
Qy       2025 GCTCATTGCTTTCAGGATGACAAAAATTTCAAGTACTCAGACTACACGATGTGGACGGCC 2084
Db       1985 GCACACTGCTACATCGATGACAGAGGATTCAGGTACTCAGACCCCACGCAGTGGACGGCC 2044
Qy       2085 TTCCTGGGTCTGCTGGACCAGAGCAAGCGCAGTGCCTCTGGGGTGCAGGAGCTGAAGCTC 2144
Db       2045 TTCCTGGGCTTGCACGACCAGAGCCAGCGCAGCGCCCCTGGGGTGCAGGAGCGCAGGCTC 2104
Qy       2145 AAACGTATCATCACCCACCCTTCCTTCAATGATTTCACCTTCGACTATGACATCGCCTTG 2204
Db       2105 AAGCGCATCATCTCCCACCCCTTCTTCAATGACTTCACCTTCGACTATGACATCGCGCTG 2164
Qy       2205 CTGGAGCTGGAGAAGTCGGTGGAGTACAGCACCGTCGTGCGCCCCATCTGCCTGCCTGAT 2264
Db       2165 CTGGAGCTGGAGAAACCGGCAGAGTACAGCTCCATGGTGCGGCCCATCTGCCTGCCGGAC 2224

Qy       2265 GCTACCCATGTCTTCCCTGCTGGCAAGGCCATCTGGGTCACAGGCTGGGGGCACACAAAA 2324
Db       2225 GCCTCCCATGTCTTCCCTGCCGGCAAGGCCATCTGGGTCACGGGCTGGGGACACACCCAG 2284
Qy       2325 GAGGGAGGTACCGGAGCGCTGATCCTGCAGAAGGGTGAGATCCGTGTCATCAACCAGACC 2384
Db       2285 TATGGAGGCACTGGCGCGCTGATCCTGCAAAAGGGTGAGATCCGCGTCATCAACCAGACC 2344
Qy       2385 ACCTGTGAGGACCTCATGCCGCAGCAGATCACCCCACGAATGATGTGTGTGGGTTTCCTC 2444
Db       2345 ACCTGCGAGAACCTCCTGCCGCAGCAGATCACGCCGCGCATGATGTGCGTGGGCTTCCTC 2404
Qy       2445 AGTGGGGGTGTGGACTCCTGCCAGGGTGACTCTGGTGGCCCCTTGTCAAGCGCGGAGAAA 2504
Db       2405 AGCGGCGGCGTGGACTCCTGCCAGGGTGATTCCGGGGGACCCCTGTCCAGCGTGGAGGCG 2464
Qy       2505 GATGGGCGAATGTTCCAGGCTGGTGTGGTGAGCTGGGGTGAAGGCTGCGCTCAGAGGAAC 2564
Db       2465 GATGGGCGGATCTTCCAGGCCGGTGTGGTGAGCTGGGGAGACGGCTGCGCTCAGAGGAAC 2524
Qy       2565 AAGCCAGGCGTGTACACAAGGCTCCCTGTAGTTCGGGACTGGATCAAAGAGCACACTGGG 2624
Db       2525 AAGCCAGGCGTGTACACAAGGCTCCCTCTGTTTCGGGACTGGATCAAAGAGAACACTGGG 2584
Qy       2625 GTATAGCAGCATGGACAGACAGCCGACCACAAACACCCACAGGGATGCCCGACATGCACA 2684
Db       2585 GTATAGGGGCCGGG---GCCACCCAAATGTGTACACCTGCGGGGCCACCCATCGTCCACC 2641
Qy       2685 CCTGGATACAGGAGAGGAACACTGACGACATTTATGCTGTGGCCTCCCCCCCCCAACACA 2744
Db       2642 CCAGTGTGCACG-CCTGCAGGCTGGAGACTGGACCGCTGACTGCACCAGCGCCC-CCAGA 2699
Qy       2745 ACCCAGACTGTGAACTGCATCCTTAGGACTCAGAGT 2780
Db       2700 ACATACACTGTGAACTCAATCTCCAGGGCTCCAAAT 2735
```
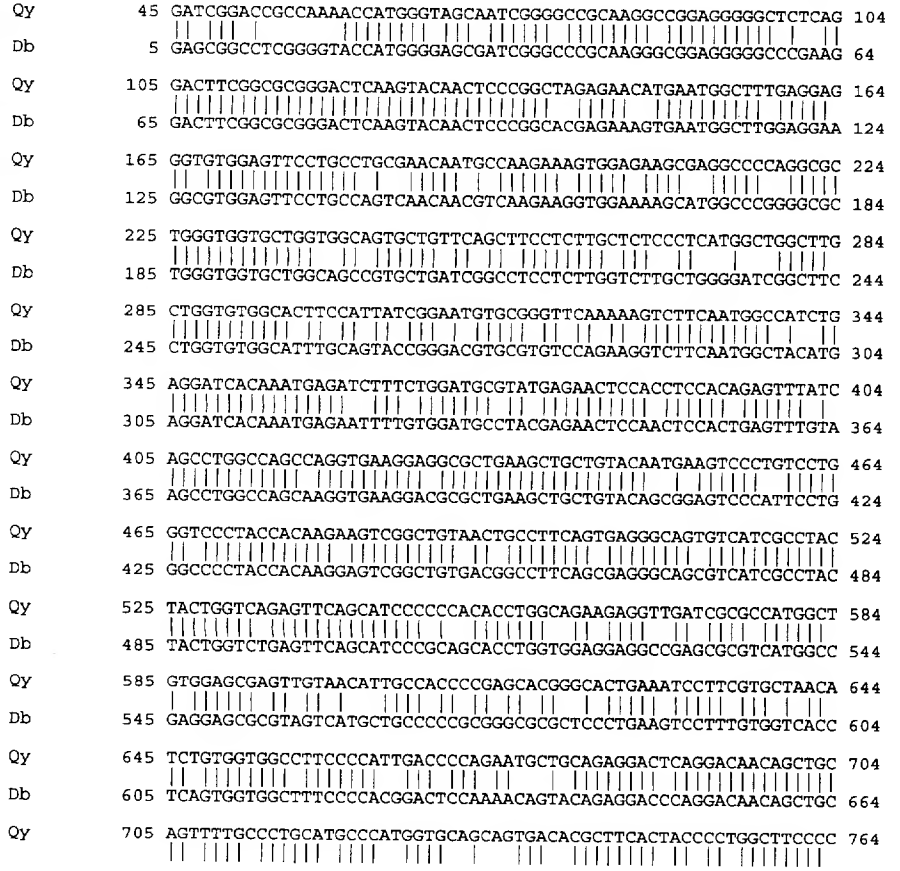
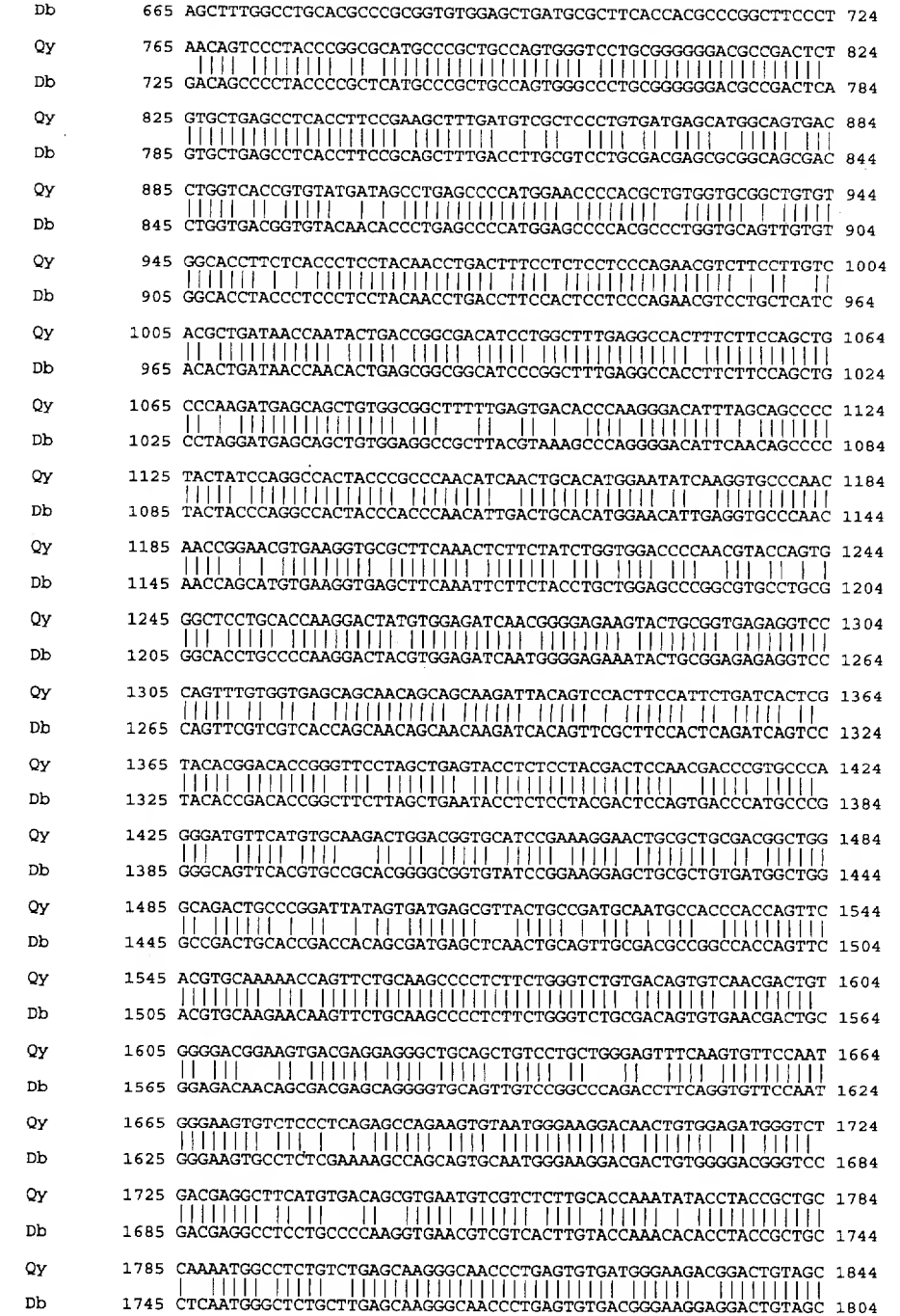

RESULT 12
ABZ58501
ID ABZ58501 standard; cDNA; 3147 BP.
XX
AC ABZ58501;
XX
DT 13-MAY-2003 (first entry)
XX
DE Transmembrane serine protease 1 (MTSP1) protein domain cDNA.
XX
KW Human; transmembrane serine protease 1; MTSP1; MTSP20; enzyme;
KW cytostatic; dermatological; cardiant; vulnerary; ophthalmological;
KW gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1865..2590
FT   /*tag= a
FT   /product= "MTSP1 protease domain"
XX
PN WO2003004681-A2.
XX
PD 16-JAN-2003.
XX
PF 03-JUL-2002; 2002WO-US21208.
XX
PR 03-JUL-2001; 2001US-302939P.
XX
PA (CORV-) CORVAS INT INC.
XX
PI Madison EL, Ong EO;
XX
DR WPI; 2003-239207/23.
DR P-PSDB; ABP72377.

XX
PT New type-II membrane-type serine protease 20 polypeptides, useful for
PT preparing a medicament for diagnosing, treating or preventing cancer,
PT dermatological disorders, aberrant wound repairs or crest syndromes -
XX
PS Disclosure; Page 200-202; 216pp; English.
XX
CC The present sequence is that of cDNA encoding the protease domain
CC of human type II transmembrane serine protease 1 (MTSP1). The
CC invention relates to novel human type II transmembrane serine protein
CC 20 (MTSP20) (see ABP72374) and nucleic acids encoding it (see
CC ABZ58499). Also claimed are methods of inhibiting tumour initiation,
CC growth or progression by inhibiting MTSP20 activity, and of treating
CC or preventing a disease or disorder associated with undesired and/or
CC uncontrolled angiogenesis or neovascularisation, especially
CC undesired angiogenesis associated with solid neoplasms, vascular
CC malformations and cardiovascular disorders, chronic inflammatory
CC diseases, aberrant wound repairs, circulatory disorders, crest
CC syndromes, dermatological disorders and ocular disorders using an
CC inhibitor of MTSP20.
XX
SQ Sequence 3147 BP; 654 A; 952 C; 958 G; 583 T; 0 other;

Query Match 60.6%; Score 1883.2; DB 25; Length 3147;
Best Local Similarity 81.2%; Pred. No. 0;
Matches 2223; Conservative 0; Mismatches 508; Indels 5; Gaps 3;





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Qy       1845 GATGGCTCCGATGAGAAAAACTGTGACTGTGGGCTGCGATCCTTTACCAAACAGGCTCGC 1904
Db       1805 GACGGCTCAGATGAGAAGGACTGCGACTGTGGGCTGCGGTCATTCACGAGACAGGCTCGT 1864

Qy       1905 GTGGTTGGTGGCACGAATGCGGACGAGGGCGAGTGGCCCTGGCAGGTGAGCCTCCACGCC 1964
Db       1865 GTTGTTGGGGGCACGGATGCGGATGAGGGCGAGTGGCCCTGGCAGGTAAGCCTGCATGCT 1924

Qy       1965 CTGGGCCAGGGCCACTTGTGTGGGGCCTCGCTCATCTCTCCTGACTGGCTGGTCTCTGCA 2024
Db       1925 CTGGGCCAGGGCCACATCTGCGGTGCTTCCCTCATCTCTCCCAACTGGCTGGTCTCTGCC 1984

Qy       2025 GCTCATTGCTTTCAGGATGACAAAAATTTCAAGTACTCAGACTACACGATGTGGACGGCC 2084
Db       1985 GCACACTGCTACATCGATGACAGAGGATTCAGGTACTCAGACCCCACGCAGTGGACGGCC 2044

Qy       2085 TTCCTGGGTCTGCTGGACCAGAGCAAGCGCAGTGCCTCTGGGGTGCAGGAGCTGAAGCTC 2144
Db       2045 TTCCTGGGCTTGCACGACCAGAGCCAGCGCAGCGCCCCTGGGGTGCAGGAGCGCAGGCTC 2104

Qy       2145 AAACGTATCATCACCCACCCTTCCTTCAATGATTTCACCTTCGACTATGACATCGCCTTG 2204
Db       2105 AAGCGCATCATCTCCCACCCCTTCTTCAATGACTTCACCTTCGACTATGACATCGCGCTG 2164

Qy       2205 CTGGAGCTGGAGAAGTCGGTGGAGTACAGCACCGTCGTGCGCCCCATCTGCCTGCCTGAT 2264
Db       2165 CTGGAGCTGGAGAAACCGGCAGAGTACAGCTCCATGGTGCGGCCCATCTGCCTGCCGGAC 2224

Qy       2265 GCTACCCATGTCTTCCCTGCTGGCAAGGCCATCTGGGTCACAGGCTGGGGGCACACAAAA 2324
Db       2225 GCCTCCCATGTCTTCCCTGCCGGCAAGGCCATCTGGGTCACGGGCTGGGGACACACCCAG 2284

Qy       2325 GAGGGAGGTACCGGAGCGCTGATCCTGCAGAAGGGTGAGATCCGTGTCATCAACCAGACC 2384
Db       2285 TATGGAGGCACTGGCGCGCTGATCCTGCAAAAGGGTGAGATCCGCGTCATCAACCAGACC 2344

Qy       2385 ACCTGTGAGGACCTCATGCCGCAGCAGATCACCCCACGAATGATGTGTGTGGGTTTCCTC 2444
Db       2345 ACCTGCGAGAACCTCCTGCCGCAGCAGATCACGCCGCGCATGATGTGCGTGGGCTTCCTC 2404

Qy       2445 AGTGGGGGTGTGGACTCCTGCCAGGGTGACTCTGGTGGCCCCTTGTCAAGCGCGGAGAAA 2504
Db       2405 AGCGGCGGCGTGGACTCCTGCCAGGGTGATTCCGGGGGACCCCTGTCCAGCGTGGAGGCG 2464

Qy       2505 GATGGGCGAATGTTCCAGGCTGGTGTGGTGAGCTGGGGTGAAGGCTGCGCTCAGAGGAAC 2564
Db       2465 GATGGGCGGATCTTCCAGGCCGGTGTGGTGAGCTGGGGAGACGGCTGCGCTCAGAGGAAC 2524

Qy       2565 AAGCCAGGCGTGTACACAAGGCTCCCTGTAGTTCGGGACTGGATCAAAGAGCACACTGGG 2624
Db       2525 AAGCCAGGCGTGTACACAAGGCTCCCTCTGTTTCGGGACTGGATCAAAGAGAACACTGGG 2584

Qy       2625 GTATAGCAGCATGGACAGACAGCCGACCACAAACACCCACAGGGATGCCCGACATGCACA 2684
Db       2585 GTATAGGGGCCGGG---GCCACCCAAATGTGTACACCTGCGGGGCCACCCATCGTCCACC 2641

Qy       2685 CCTGGATACAGGAGAGGAACACTGACGACATTTATGCTGTGGCCTCCCCCCCCCAACACA 2744
Db       2642 CCAGTGTGCACG-CCTGCAGGCTGGAGACTGGACCGCTGACTGCACCAGCGCCC-CCAGA 2699

Qy       2745 ACCCAGACTGTGAACTGCATCCTTAGGACTCAGAGT 2780
Db       2700 ACATACACTGTGAACTCAATCTCCAGGGCTCCAAAT 2735
```

```
RESULT 13
ABZ22450
ID   ABZ22450 standard; cDNA; 3147 BP.
XX
AC   ABZ22450;
XX
DT   24-MAR-2003  (first entry)
XX
DE   Human membrane-type serine protease MTSP1 encoding cDNA SEQ ID NO:1.
XX
KW   Human; membrane-type serine protease; enzyme; MTSP10; cytostatic;
KW   type-II membrane-type serine protease; neoplastic disease; tumour;
KW   MTSP1; matriptase; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             23..2590
FT                   /*tag=  a
FT                   /product= "membrane-type serine protease MTSP1"
FT                   /note= "also known as matriptase"
XX
PN   WO200292841-A2.
XX
PD   21-NOV-2002.
XX
PF   14-MAY-2002; 2002WO-US15332.
XX
PR   14-MAY-2001; 2001US-291001P.
XX
PA   (CORV-) CORVAS INT INC.
XX
PI   Madison EL,  Yeh J;
XX
DR   WPI; 2003-129309/12.
DR   P-PSDB; ABP56619.
XX
PT   New polypeptides comprising the protease domain of a type-II
PT   membrane-type serine protease (MTSP10), or its muteins, useful for
PT   diagnosing neoplasms or malignancies, or for screening for MTSP10
PT   inhibitors for treating such diseases  -
XX
PS   Example 1; Page 177-181; 198pp; English.
XX
CC   The present invention describes a polypeptide comprising a purified
CC   single or two chain polypeptide, which comprises the protease domain of
CC   a type-II membrane-type serine protease (MTSP10) or its catalytically
CC   active portion, or a mutein of it, where up to 50 % of the amino acids
CC   are replaced with another amino acid, and the resulting polypeptide is a
CC   single chain or two chain polypeptide that has a catalytic activity of
CC   at least 1-10 % of the unmutated polypeptide. MTSP10 has cytostatic
CC   activity. The polypeptide containing the protease domain of the MTSP10
CC   is useful for detecting a neoplastic disease, and for diagnosing the
CC   presence of a pre-malignant lesion, a malignancy, or other pathologic
CC   condition in a subject, or monitoring tumour (e.g. breast, cervix,
CC   prostate, lung, ovary or colon tumour) progression and/or therapeutic
CC   effectiveness. An inhibitor of the polypeptide containing the protease
CC   domain of MTSP10 is useful for treating or preventing neoplastic disease
CC   in a mammal. An inhibitor of the activation cleavage of the zymogen
CC   form of the MTSP10 polypeptide is useful for inhibiting tumour
CC   initiation, growth or progression, or treating (pre-)malignant conditions
CC   of the e.g. breast, cervix, prostate, lung, ovary or colon. The present
CC   sequence encodes human MTSP1 (also known as matriptase), which is used
CC   in an example from the present invention.
XX
SQ   Sequence 3147 BP; 654 A; 952 C; 958 G; 583 T; 0 other;
```

```
  Query Match             60.6%;  Score 1883.2;  DB 25;  Length 3147;
  Best Local Similarity   81.2%;  Pred. No. 0;
  Matches 2223;  Conservative    0;  Mismatches  508;  Indels    5;  Gaps    3;

Qy         45 GATCGGACCGCCAAAACCATGGGTAGCAATCGGGGCCGCAAGGCCGGAGGGGGCTCTCAG 104
Db          5 GAGCGGCCTCGGGGTACCATGGGGAGCGATCGGGCCCGCAAGGGCGGAGGGGGCCCGAAG 64

Qy        105 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCTAGAGAACATGAATGGCTTTGAGGAG 164
Db         65 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCACGAGAAAGTGAATGGCTTGGAGGAA 124

Qy        165 GGTGTGGAGTTCCTGCCTGCGAACAATGCCAAGAAAGTGGAGAAGCGAGGCCCCAGGCGC 224
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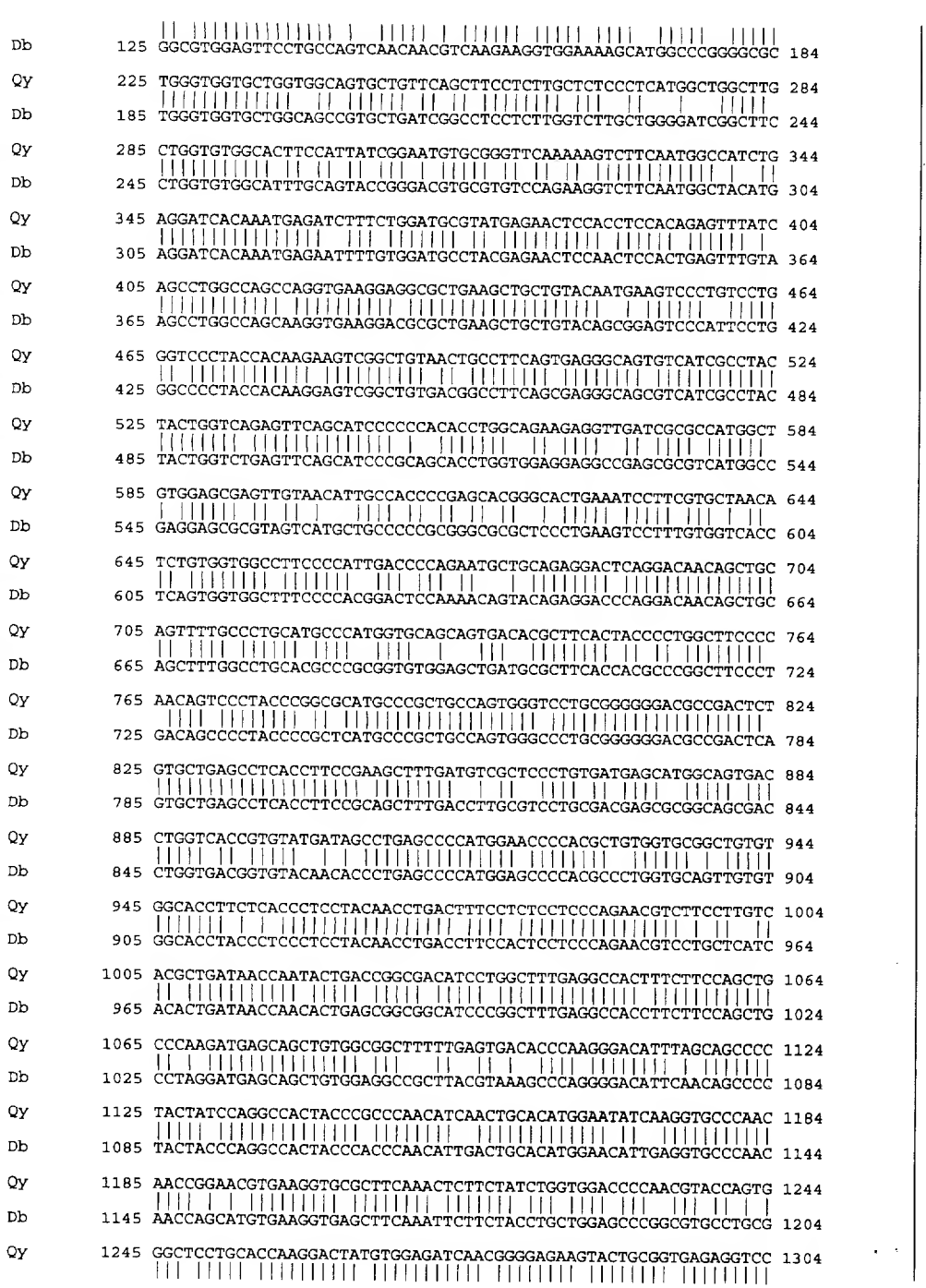

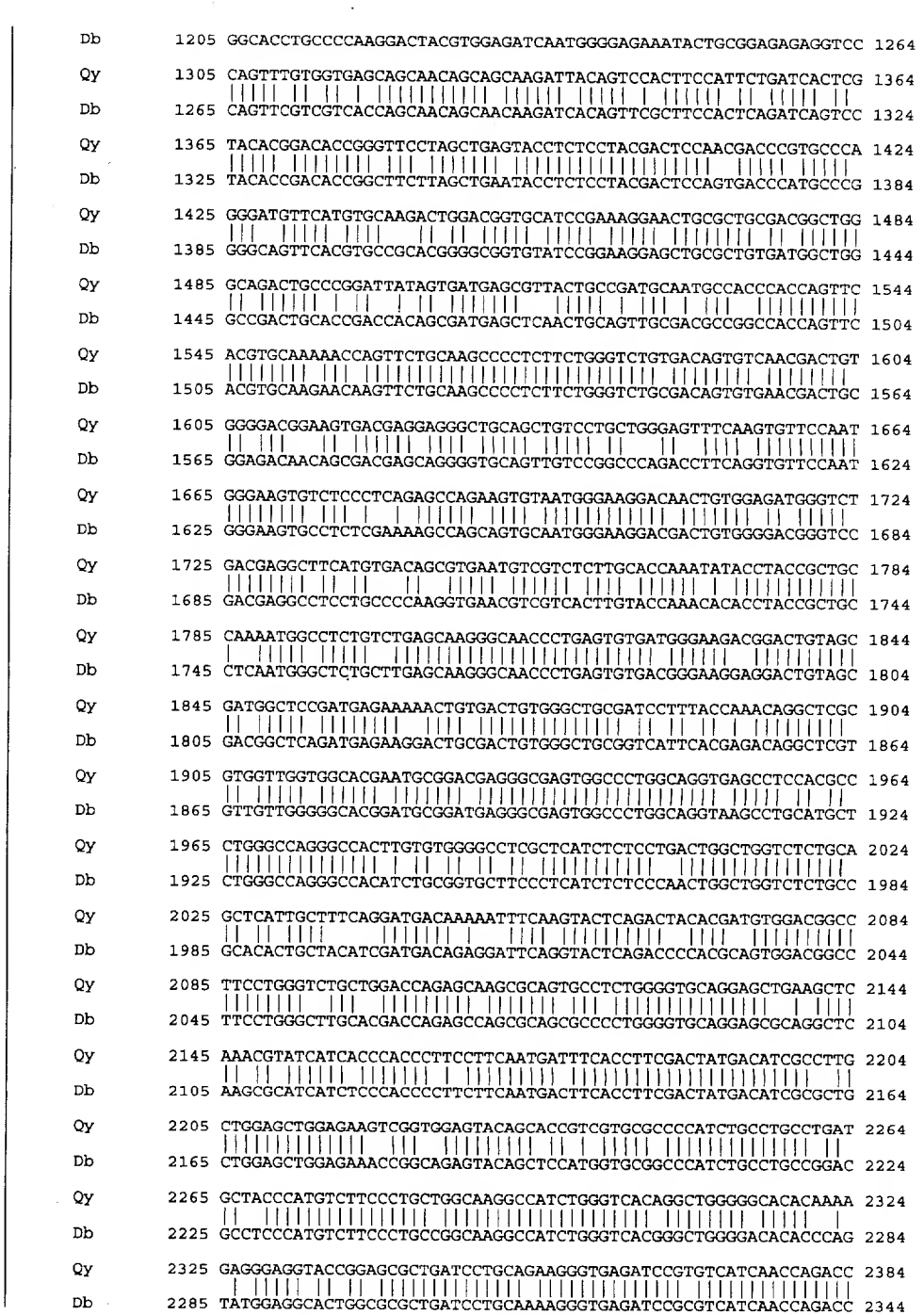

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Qy       2385 ACCTGTGAGGACCTCATGCCGCAGCAGATCACCCCACGAATGATGTGTGTGGGTTTCCTC 2444
Db       2345 ACCTGCGAGAACCTCCTGCCGCAGCAGATCACGCCGCGCATGATGTGCGTGGGCTTCCTC 2404

Qy       2445 AGTGGGGGTGTGGACTCCTGCCAGGGTGACTCTGGTGGCCCCCTTGTCAAGCGCGGAGAAA 2504
Db       2405 AGCGGCGGCGTGGACTCCTGCCAGGGTGATTCCGGGGGACCCCTGTCCAGCGTGGAGGCG 2464

Qy       2505 GATGGGCGAATGTTCCAGGCTGGTGTGGTGAGCTGGGGTGAAGGCTGCGCTCAGAGGAAC 2564
Db       2465 GATGGGCGGATCTTCCAGGCCGGTGTGGTGAGCTGGGGAGACGGCTGCGCTCAGAGGAAC 2524

Qy       2565 AAGCCAGGCGTGTACACAAGGCTCCCTGTAGTTCGGGACTGGATCAAAGAGCACACTGGG 2624
Db       2525 AAGCCAGGCGTGTACACAAGGCTCCCTCTGTTTCGGGACTGGATCAAAGAGAACACTGGG 2584

Qy       2625 GTATAGCAGCATGGACAGACAGCCGACCACAAACACCCACAGGGATGCCCGACATGCACA 2684
Db       2585 GTATAGGGGCCGGG---GCCACCCAAATGTGTACACCTGCGGGGCCACCCATCGTCCACC 2641

Qy       2685 CCTGGATACAGGAGAGGAACACTGACGACATTTATGCTGTGGCCTCCCCCCCCCAACACA 2744
Db       2642 CCAGTGTGCACG-CCTGCAGGCTGGAGACTGGACCGCTGACTGCACCAGCGCCC-CCAGA 2699

Qy       2745 ACCCAGACTGTGAACTGCATCCTTAGGACTCAGAGT 2780
Db       2700 ACATACACTGTGAACTCAATCTCCAGGGCTCCAAAT 2735
```

RESULT 14
ABZ22451
ID ABZ22451 standard; cDNA; 3147 BP.
XX
AC ABZ22451;
XX
DT 24-MAR-2003 (first entry)
XX
DE Human MTSP1 protease domain encoding cDNA SEQ ID NO:3.
XX
KW Human; membrane-type serine protease; enzyme; MTSP10; cytostatic;
KW type-II membrane-type serine protease; neoplastic disease; tumour;
KW MTSP1; matriptase; gene; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1865..2590
FT   /*tag= a
FT   /partial
FT   /product= "MTSP1 protease domain"
FT   /note= "no start codon given"
XX
PN WO200292841-A2.
XX
PD 21-NOV-2002.
XX
PF 14-MAY-2002; 2002WO-US15332.
XX
PR 14-MAY-2001; 2001US-291001P.
XX
PA (CORV-) CORVAS INT INC.
XX
PI Madison EL, Yeh J;
XX
DR WPI; 2003-129309/12.
DR P-PSDB; ABP56620.
XX
PT New polypeptides comprising the protease domain of a type-II
PT membrane-type serine protease (MTSP10), or its muteins, useful for
PT diagnosing neoplasms or malignancies, or for screening for MTSP10
PT inhibitors for treating such diseases -
XX
PS Example 1; Page 183-185; 198pp; English.
XX
CC The present invention describes a polypeptide comprising a purified
CC single or two chain polypeptide, which comprises the protease domain of
CC a type-II membrane-type serine protease (MTSP10) or its catalytically
CC active portion, or a mutein of it, where up to 50 % of the amino acids
CC are replaced with another amino acid, and the resulting polypeptide is a
CC single chain or two chain polypeptide that has a catalytic activity of
CC at least 1-10 % of the unmutated polypeptide. MTSP10 has cytostatic
CC activity. The polypeptide containing the protease domain of the MTSP10
CC is useful for detecting a neoplastic disease, and for diagnosing the
CC presence of a pre-malignant lesion, a malignancy, or other pathologic
CC condition in a subject, or monitoring tumour (e.g. breast, cervix,
CC prostate, lung, ovary or colon tumour) progression and/or therapeutic
CC effectiveness. An inhibitor of the polypeptide containing the protease
CC domain of MTSP10 is useful for treating or preventing neoplastic disease
CC in a mammal. An inhibitor of the activation cleavage of the zymogen
CC form of the MTSP10 polypeptide is useful for inhibiting tumour
CC initiation, growth or progression, or treating (pre-)malignant conditions
CC of the e.g. breast, cervix, prostate, lung, ovary or colon. The present
CC sequence encodes the protease domain of human MTSP1 (also known as
CC matriptase), which is used in an example from the present invention.
XX
SQ Sequence 3147 BP; 654 A; 952 C; 958 G; 583 T; 0 other;

Query Match 60.6%; Score 1883.2; DB 25; Length 3147;
Best Local Similarity 81.2%; Pred. No. 0;
Matches 2223; Conservative 0; Mismatches 508; Indels 5; Gaps 3;

```
Qy         45 GATCGGACCGCCAAAACCATGGGTAGCAATCGGGGCCGCAAGGCCGGAGGGGGCTCTCAG 104
Db          5 GAGCGGCCTCGGGGTACCATGGGGAGCGATCGGGCCCGCAAGGGCGGAGGGGGCCCGAAG 64

Qy        105 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCTAGAGAACATGAATGGCTTTGAGGAG 164
Db         65 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCACGAGAAAGTGAATGGCTTGGAGGAA 124

Qy        165 GGTGTGGAGTTCCTGCCTGCGAACAATGCCAAGAAAGTGGAGAAGCGAGGCCCCAGGCGC 224
Db        125 GGCGTGGAGTTCCTGCCAGTCAACAACGTCAAGAAGGTGGAAAAGCATGGCCCGGGGCGC 184

Qy        225 TGGGTGGTGCTGGTGGCAGTGCTGTTCAGCTTCCTCTTGCTCTCCCTCATGGCTGGCTTG 284
Db        185 TGGGTGGTGCTGGCAGCCGTGCTGATCGGCCTCCTCTTGGTCTTGCTGGGGATCGGCTTC 244

Qy        285 CTGGTGTGGCACTTCCATTATCGGAATGTGCGGGTTCAAAAAGTCTTCAATGGCCATCTG 344
Db        245 CTGGTGTGGCATTTGCAGTACCGGGACGTGCGTGTCCAGAAGGTCTTCAATGGCTACATG 304

Qy        345 AGGATCACAAATGAGATCTTTCTGGATGCGTATGAGAACTCCACCTCCACAGAGTTTATC 404
Db        305 AGGATCACAAATGAGAATTTTGTGGATGCCTACGAGAACTCCAACTCCACTGAGTTTGTA 364

Qy        405 AGCCTGGCCAGCCAGGTGAAGGAGGCGCTGAAGCTGCTGTACAATGAAGTCCCTGTCCTG 464
Db        365 AGCCTGGCCAGCAAGGTGAAGGACGCGCTGAAGCTGCTGTACAGCGGAGTCCCATTCCTG 424

Qy        465 GGTCCCTACCACAAGAAGTCGGCTGTAACTGCCTTCAGTGAGGGCAGTGTCATCGCCTAC 524
Db        425 GGCCCCTACCACAAGGAGTCGGCTGTGACGGCCTTCAGCGAGGGCAGCGTCATCGCCTAC 484

Qy        525 TACTGGTCAGAGTTCAGCATCCCCCCACACCTGGCAGAAGAGGTTGATCGCGCCATGGCT 584
Db        485 TACTGGTCTGAGTTCAGCATCCCGCAGCACCTGGTGGAGGAGGCCGAGCGCGTCATGGCC 544

Qy        585 GTGGAGCGAGTTGTAACATTGCCACCCCGAGCACGGGCACTGAAATCCTTCGTGCTAACA 644
Db        545 GAGGAGCGCGTAGTCATGCTGCCCCCGCGGGCGCGCTCCCTGAAGTCCTTTGTGGTCACC 604

Qy        645 TCTGTGGTGGCCTTCCCCATTGACCCCAGAATGCTGCAGAGGACTCAGGACAACAGCTGC 704
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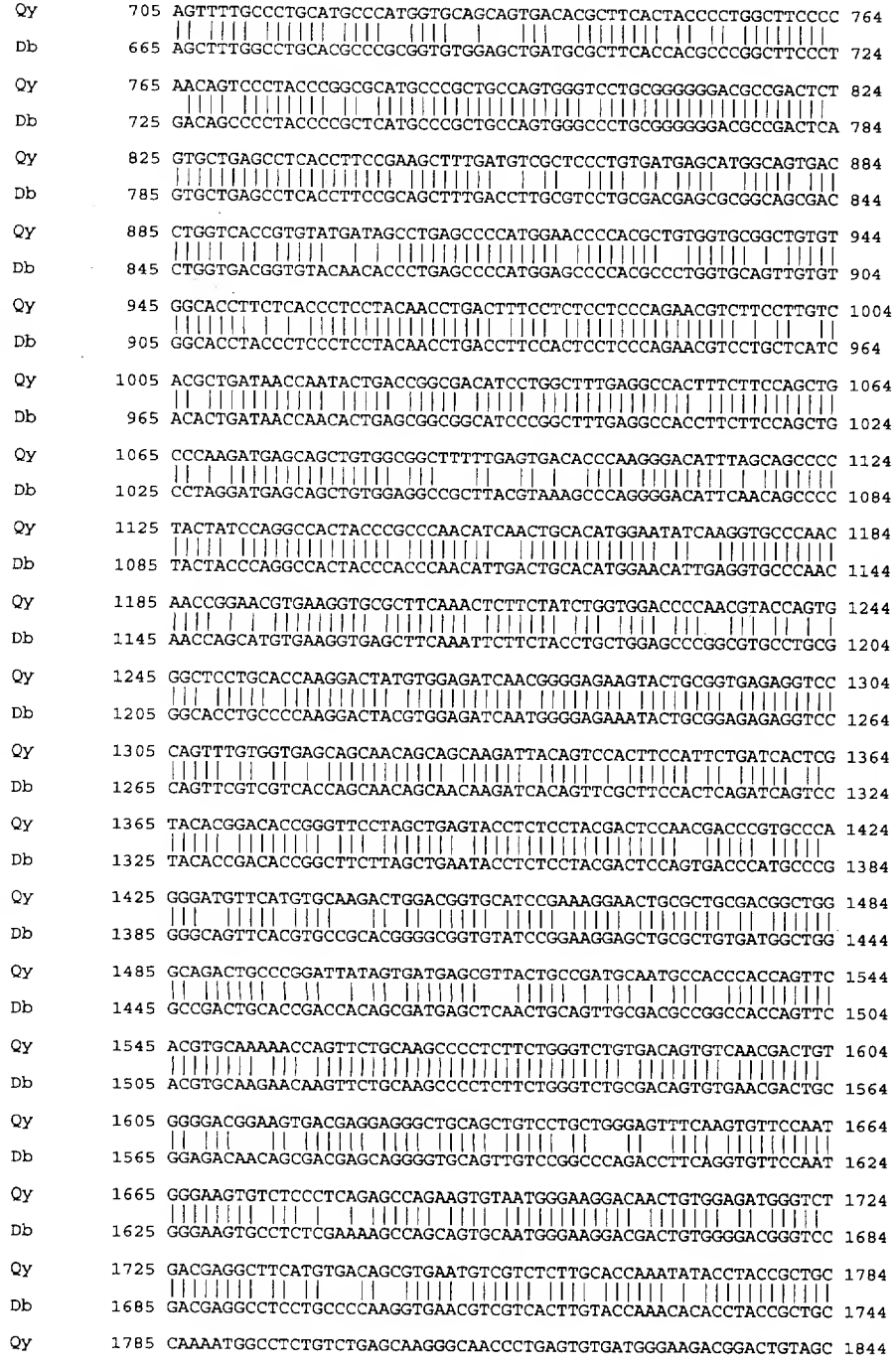

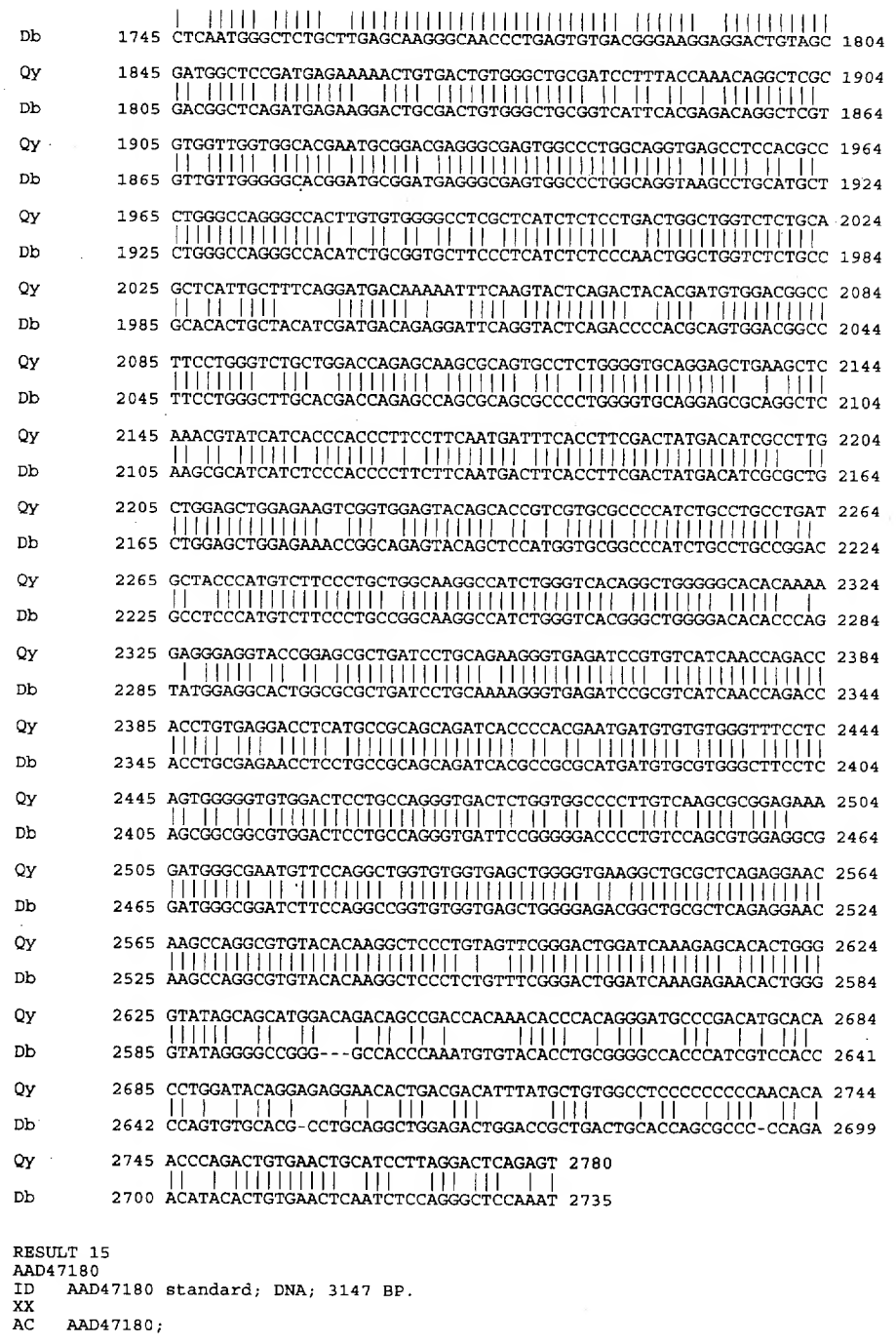

RESULT 15
AAD47180
ID AAD47180 standard; DNA; 3147 BP.
XX
AC AAD47180;

```
XX
DT   24-FEB-2003  (first entry)
XX
DE   Human membrane-type serine protease, MTSP1 DNA.
XX
KW   Human; serine protease 14; CVSP14; cancer; malignancy; breast; colon;
KW   gene therapy; cytostatic; membrane-type serine protease; enzyme; MTSP1;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             23..2590
FT                   /*tag= a
FT                   /product= "Human MTSP1 protein"
XX
PN   WO200277263-A2.
XX
PD   03-OCT-2002.
XX
PF   20-MAR-2002; 2002WO-US09039.
XX
PR   22-MAR-2001; 2001US-278166P.
XX
PA   (CORV-) CORVAS INT INC.
XX
PI   Madison EL,  Yeh J;
XX
DR   WPI; 2003-018938/01.
DR   P-PSDB; AAE29791.
XX
PT   New purified CVSP14 polypeptide and encoding nucleic acid molecule,
PT   useful for diagnosing, preventing and/or treating disorders, such as
PT   cancers and malignancies of the breast, cervix, prostate, lung, ovary
PT   or colon  -
XX
PS   Disclosure; Page 167-171; 185pp; English.
XX
CC   The invention relates to transmembrane serine protease 14 (CVSP14), its
CC   nucleic acid sequence and the method based on them. The methods and
CC   compositions of the invention are useful for diagnosing, preventing
CC   and/or treating conditions associated with the aberrant expression or
CC   activity of the CVSP14 polypeptide, such as cancers and malignancies of
CC   the breast, cervix, prostate, lung, ovary or colon. The methods are
CC   also useful for identifying compounds that will modulate the protease
CC   activity of CVSP14 polypeptide, and monitoring tumour progression and/or
CC   therapeutic effectiveness. CVSP14 DNA used in gene therapy. The present
CC   sequence is human membrane-type serine protease, MTSP1 DNA.
XX
SQ   Sequence 3147 BP; 654 A; 952 C; 958 G; 583 T; 0 other;

  Query Match           60.6%;  Score 1883.2;  DB 25;  Length 3147;
  Best Local Similarity  81.2%;  Pred. No. 0;
  Matches 2223;  Conservative    0;  Mismatches  508;  Indels    5;  Gaps    3;

Qy        45 GATCGGACCGCCAAAACCATGGGTAGCAATCGGGGCCGCAAGGCCGGAGGGGGCTCTCAG 104
             ||  |||  |       |||||||| ||| |||||| |||||||| |||||||||| |  ||
Db         5 GAGCGGCCTCGGGGTACCATGGGGAGCGATCGGGCCCGCAAGGGCGGAGGGGGCCCGAAG 64

Qy       105 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCTAGAGAACATGAATGGCTTTGAGGAG 164
             |||||||||||||||||||||||||||||||  |||||  |||||||||| |||||
Db        65 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCACGAGAAAGTGAATGGCTTGGAGGAA 124

Qy       165 GGTGTGGAGTTCCTGCCTGCGAACAATGCCAAGAAAGTGGAGAAGCGAGGCCCCAGGCGC 224
             ||  |||||||||||||  |  |||||  |  |||||  |||||  ||||   |||||  |||||
Db       125 GGCGTGGAGTTCCTGCCAGTCAACAACGTCAAGAAGGTGGAAAAGCATGGCCCGGGGCGC 184

Qy       225 TGGGTGGTGCTGGTGGCAGTGCTGTTCAGCTTCCTCTTGCTCTCCCTCATGGCTGGCTTG 284
             |||||||||||||  ||  ||||||  ||  ||  ||||||| |||  ||   |  |||||
Db       185 TGGGTGGTGCTGGCAGCCGTGCTGATCGGCCTCCTCTTGGTCTTGCTGGGGATCGGCTTC 244

Qy       285 CTGGTGTGGCACTTCCATTATCGGAATGTGCGGGTTCAAAAAGTCTTCAATGGCCATCTG 344
             ||||||||||| ||  ||  ||  |||  |  |||||  ||  ||  ||  ||||||||||||  |  ||

Db       245 CTGGTGTGGCATTTGCAGTACCGGGACGTGCGTGTCCAGAAGGTCTTCAATGGCTACATG 304

Qy       345 AGGATCACAAATGAGATCTTTCTGGATGCGTATGAGAACTCCACCTCCACAGAGTTTATC 404
             ||||||||||||||||  |||  |||||||  ||  |||||||||  ||||||  ||||||  |
Db       305 AGGATCACAAATGAGAATTTTGTGGATGCCTACGAGAACTCCAACTCCACTGAGTTTGTA 364

Qy       405 AGCCTGGCCAGCCAGGTGAAGGAGGCGCTGAAGCTGCTGTACAATGAAGTCCCTGTCCTG 464
             ||||||||||||  ||||||||||  ||||||||||||||||||||  |  ||||||  |||||
Db       365 AGCCTGGCCAGCAAGGTGAAGGACGCGCTGAAGCTGCTGTACAGCGGAGTCCCATTCCTG 424

Qy       465 GGTCCCTACCACAAGAAGTCGGCTGTAACTGCCTTCAGTGAGGGCAGTGTCATCGCCTAC 524
             ||  ||||||||||||  ||||||||||  ||  ||||||||  |||||||  |||||||||||
Db       425 GGCCCCTACCACAAGGAGTCGGCTGTGACGGCCTTCAGCGAGGGCAGCGTCATCGCCTAC 484

Qy       525 TACTGGTCAGAGTTCAGCATCCCCCCACACCTGGCAGAAGAGGTTGATCGCGCCATGGCT 584
             |||||||  ||||||||||||||  |  |||||||  ||  |||  ||  ||||  ||||||
Db       485 TACTGGTCTGAGTTCAGCATCCCGCAGCACCTGGTGGAGGAGGCCGAGCGCGTCATGGCC 544

Qy       585 GTGGAGCGAGTTGTAACATTGCCACCCCGAGCACGGGCACTGAAATCCTTCGTGCTAACA 644
             |  ||||||  ||  ||  |   ||||  ||  ||  ||  ||  |  |||||  |||||  |||  |  ||
Db       545 GAGGAGCGCGTAGTCATGCTGCCCCCGCGGGCGCGCTCCCTGAAGTCCTTTGTGGTCACC 604

Qy       645 TCTGTGGTGGCCTTCCCCATTGACCCCAGAATGCTGCAGAGGACTCAGGACAACAGCTGC 704
             ||  |||||||  |||||||  |||  |||  ||    |  ||||||||  ||||||||||||||||
Db       605 TCAGTGGTGGCTTTCCCCACGGACTCCAAAACAGTACAGAGGACCCAGGACAACAGCTGC 664

Qy       705 AGTTTTGCCCTGCATGCCCATGGTGCAGCAGTGACACGCTTCACTACCCCTGGCTTCCCC 764
             ||  ||||  ||||||  |||||  ||||  |  |||  ||||||||  ||  ||  ||||||||
Db       665 AGCTTTGGCCTGCACGCCCGCGGTGTGGAGCTGATGCGCTTCACCACGCCCGGCTTCCCT 724

Qy       765 AACAGTCCCTACCCGGCGCATGCCCGCTGCCAGTGGGTCCTGCGGGGGGGACGCCGACTCT 824
             ||||  ||||||||  ||  ||||||||||||||||||  ||||||||||||||||||||
Db       725 GACAGCCCCTACCCCGCTCATGCCCGCTGCCAGTGGGCCCTGCGGGGGGGACGCCGACTCA 784

Qy       825 GTGCTGAGCCTCACCTTCCGAAGCTTTGATGTCGCTCCCTGTGATGAGCATGGCAGTGAC 884
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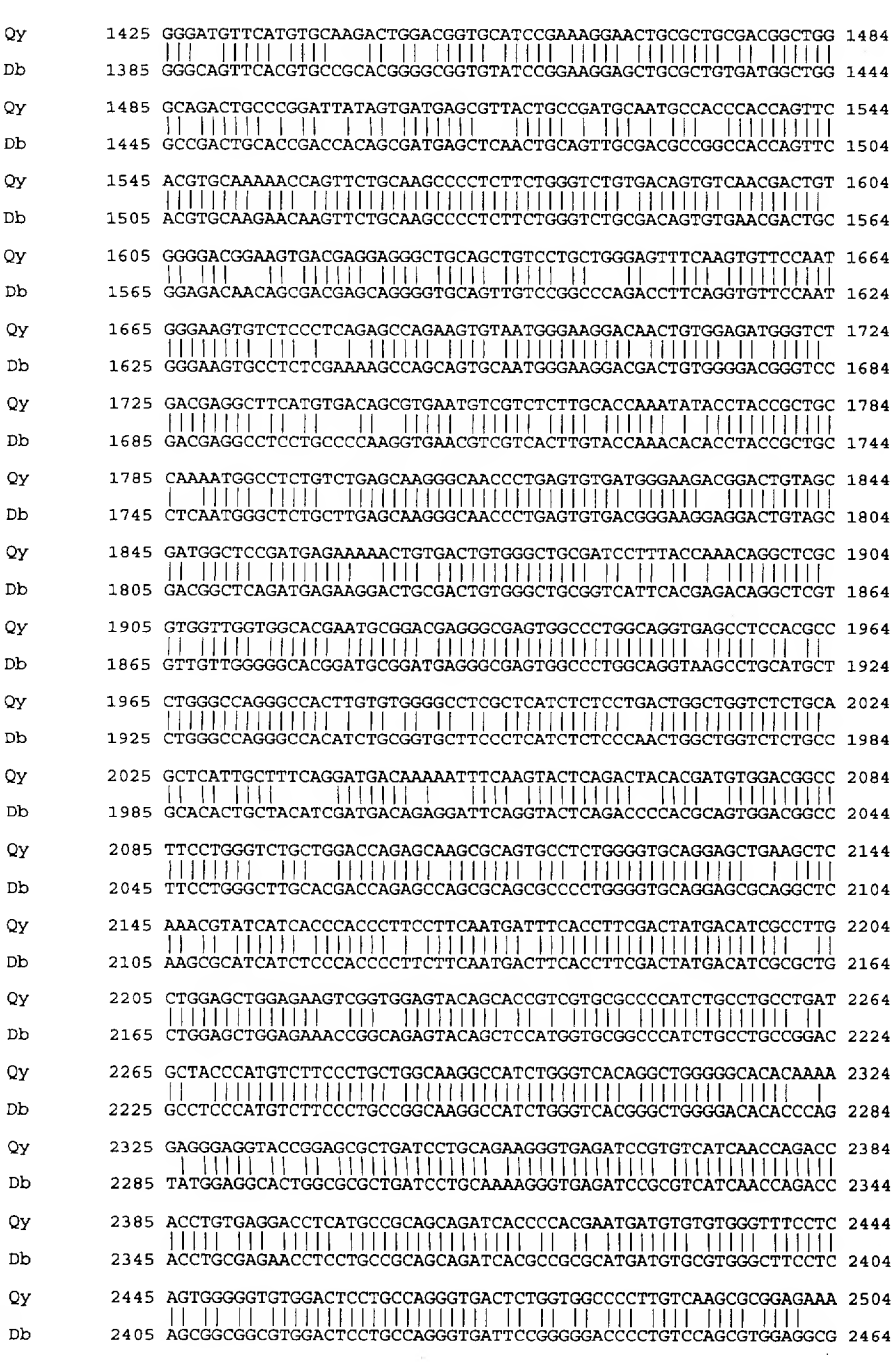

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	6	701.2	22.6	1553	4	US-09-280-116-10	Sequence 10, Appl
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ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/09027337B
; Patent No. 5972616
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotoshi
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease Overexpressed in
; TITLE OF INVENTION: Breast and Ovarian Carcinomas
; FILE REFERENCE: D6064
; CURRENT APPLICATION NUMBER: US/09/027,337B
; CURRENT FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 1
; LENGTH: 3147
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: 23..2589
; OTHER INFORMATION: cDNA sequence of TADG-15
US-09-027-337-1

Query Match 60.6%; Score 1883.2; DB 2; Length 3147;
Best Local Similarity 81.2%; Pred. No. 0;
Matches 2223; Conservative 0; Mismatches 508; Indels 5; Gaps 3;

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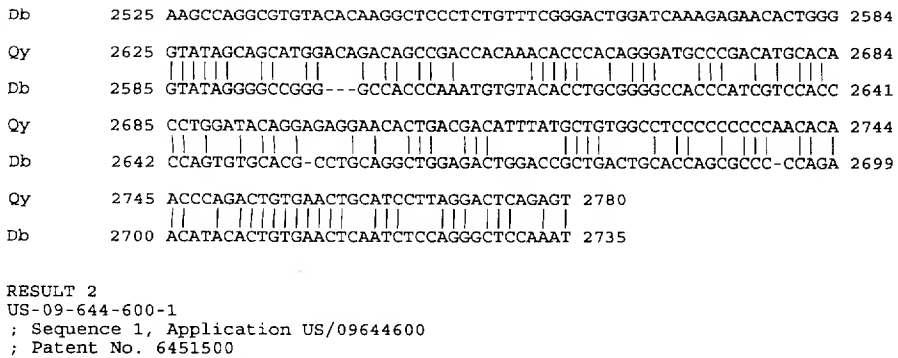

RESULT 2
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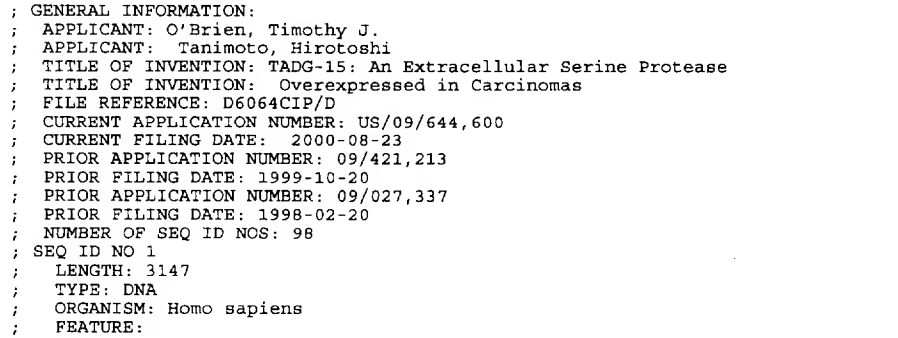
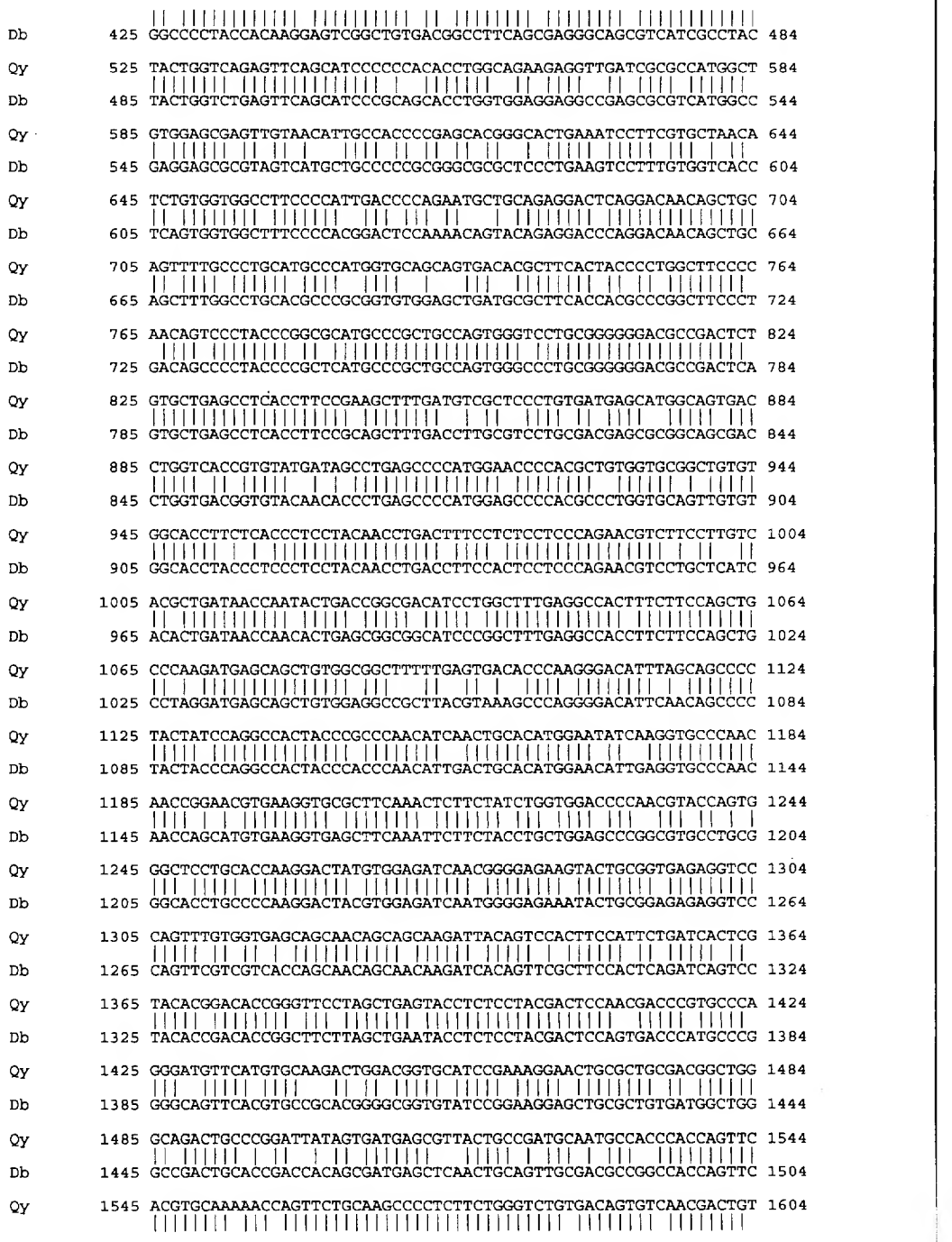
; Sequence 1, Application US/09644600
; Patent No. 6451500
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotoshi
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
; TITLE OF INVENTION: Overexpressed in Carcinomas
; FILE REFERENCE: D6064CIP/D
; CURRENT APPLICATION NUMBER: US/09/644,600
; CURRENT FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/421,213
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: 09/027,337
; PRIOR FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 1
; LENGTH: 3147
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TADG-15
US-09-644-600-1

Query Match 60.6%; Score 1883.2; DB 4; Length 3147;
Best Local Similarity 81.2%; Pred. No. 0;
Matches 2223; Conservative 0; Mismatches 508; Indels 5; Gaps 3;





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; Sequence 18, Application US/09644600
; Patent No. 6451500
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotoshi
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
; TITLE OF INVENTION: Overexpressed in Carcinomas
; FILE REFERENCE: D6064CIP/D
; CURRENT APPLICATION NUMBER: US/09/644,600
; CURRENT FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/421,213
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: 09/027,337
; PRIOR FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 18
; LENGTH: 3147
; TYPE: RNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Antisense of TADG-15
US-09-644-600-18

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Best Local Similarity 81.2%; Pred. No. 0;
Matches 2223; Conservative 0; Mismatches 508; Indels 5; Gaps 3;

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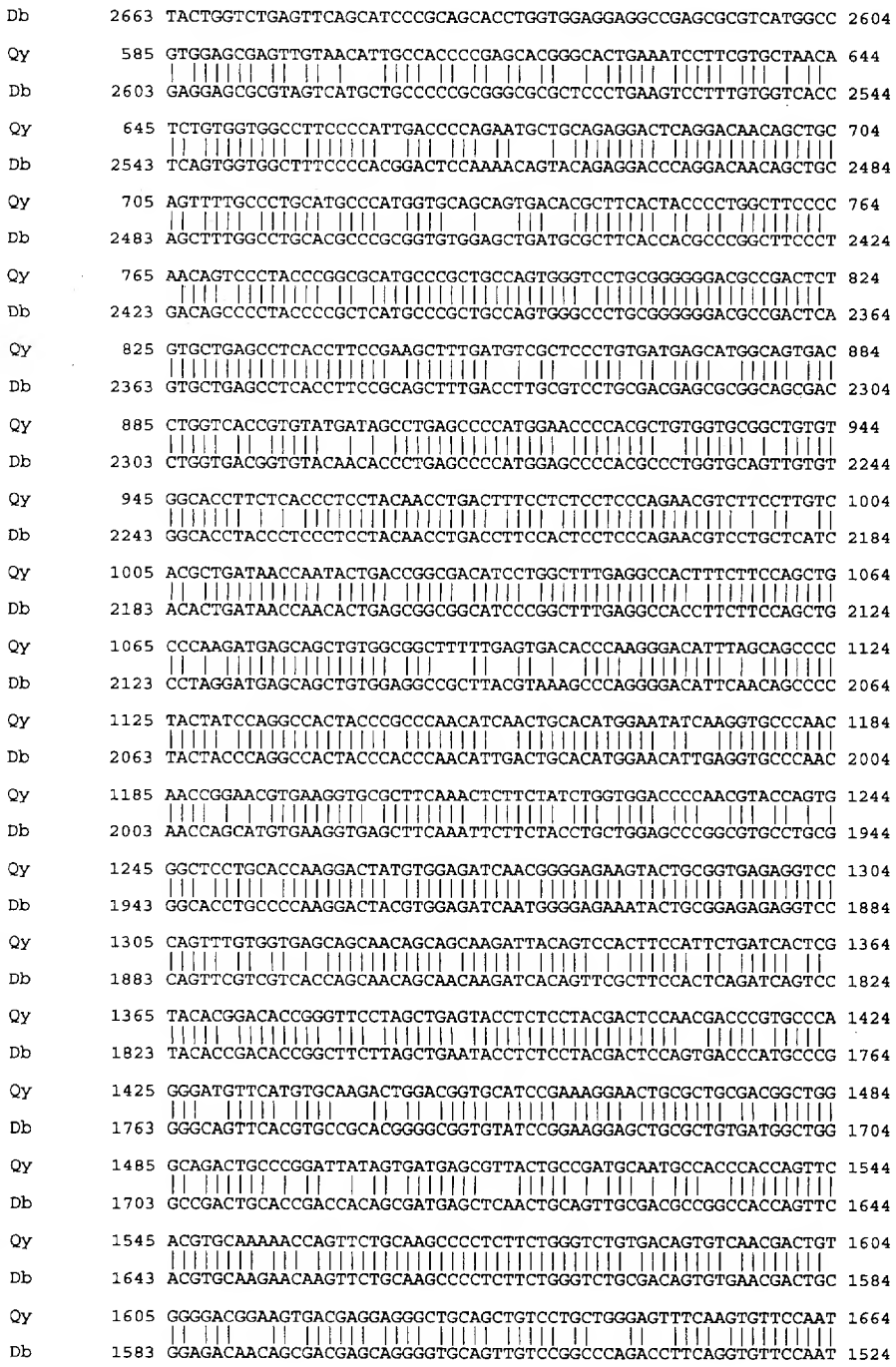
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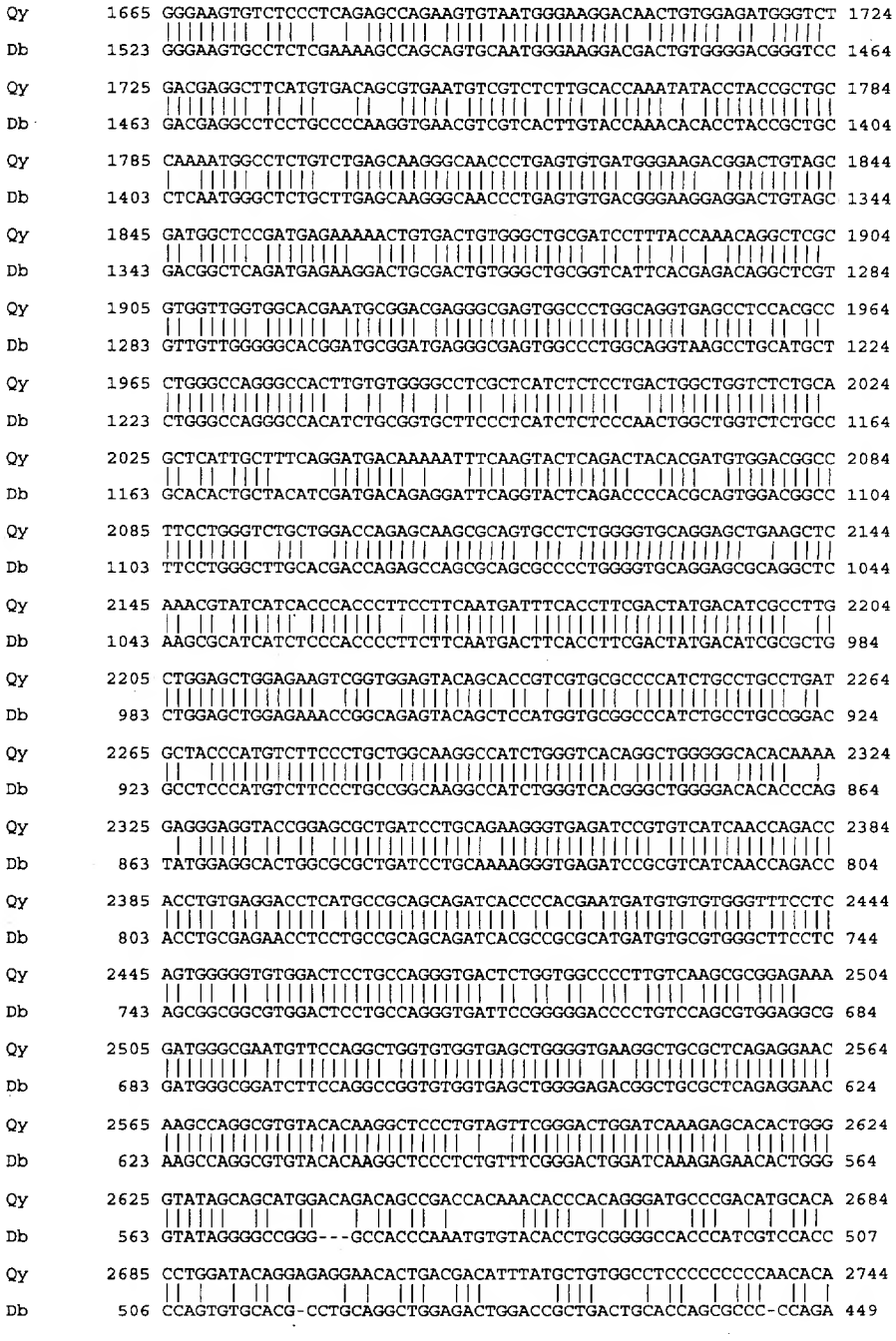
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Db 743 AGCGGCGGCGTGGACTCCTGCCAGGGTGATTCCGGGGGACCCCTGTCCAGCGTGGAGGCG 684
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Qy 2625 GTATAGCAGCATGGACAGACAGCCGACCACAAACACCCACAGGGATGCCCGACATGCACA 2684
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RESULT 4
US-09-027-337-9
; Sequence 9, Application US/09027337B
; Patent No. 5972616
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotoshi
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease Overexpressed in
; TITLE OF INVENTION: Breast and Ovarian Carcinomas
; FILE REFERENCE: D6064
; CURRENT APPLICATION NUMBER: US/09/027,337B
; CURRENT FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 9
; LENGTH: 2900
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: SNC19 mRNA sequence (U20428)
US-09-027-337-9

Query Match 49.3%; Score 1530.8; DB 2; Length 2900;
Best Local Similarity 79.1%; Pred. No. 0;
Matches 2011; Conservative 0; Mismatches 502; Indels 29; Gaps 15;

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Qy        282 TTGCTGGTGTGGCACTTCCATTATCGGAATGTGCGGGTTCAAAAAGTCTTCAATGGCCAT 341
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Qy        402 ATCAGCCTGGCCAGCCAGGTGAAGGAGGCGCTGAAGCTGCTGTACAATGAAGTCCCTGTC 461
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Qy        522 TACTACTGGTCAGAGTTCAGCATCCCCCCACACCTGGCAGAAGAGGTTGATCGCGCCATG 581
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Qy        582 GCTGTGGAGCGAGTTGTAACATTGCCACCCCGAGCACGGGCACTGAAATCCTTCGTGCTA 641
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Qy        642 ACATCTGTGGTGGCCTTCCCCATTGACCCCAGAATGCTGCAGAGGACTCAGGACAACAGC 701
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Qy        702 TGCAGTTTTGCCCTGCATGCCCATGGTGCAGCAGTGACACGCTTCACTACCCCTGGCTTC 761
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Qy        762 CCCAACAGTCCCTACCCGGCGCATGCCCGCTGCCAGTGGGTCCTGCGGGGGGACGCCGAC 821
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Qy        882 GACCTGGTCACCGTGTATGATAGCCTGAGCCCCATGGAACCCCACGCTGTGGTGCGGCTG 941
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Qy        942 TGTGGCACCTTCTCACCCTCCTACAACCTGACTTTCCTCTCC--TCCCAGAACGTCTTCC 999
Db        709 TGTGGCACCTACCCTCCCTCCTACAACCTGACCTTCCACTCCCTCCCACGAACGTCCTGC 768

Qy       1000 TTGTCACGCTGATAACCAATACTGACCGGCGACATCCTGGCTTTGAGGCCACTTTCTTCC 1059
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Qy       1060 AGCTGCCCAAGATGAGCAGCTGTGGCGGCTTTTTGAGTGACACCCAAGGGACATTTAGCA 1119
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Qy       1120 GCCCCTACTATCCAGGCCACTACCCGCCCAACATCAACTGCACATGGAATATCAAGGTGC 1179
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Qy       1180 CCAACAACCGGAACGTGAAGGTGCGCTTCAAACTCTTCTATCTGGTGGACCCCAACGTAC 1239
Db        947 CCAACAACCAGCATGTGAAGGTGCGCTTCAAATTCTTCTACCTGCTGGAGCCCGGCGTGC 1006

Qy       1240 CAGTGGGCTCCTGCACCAAGGACTATGTGGAGATCAACGGGGAGAAGTACTGCGGTGAGA 1299
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Qy       1659 TCCAATGGGAAGTGTCTCCCTCAGAGCCAGAAGTGTAATGGGAAGGACAACTGTGGAGAT 1718
Db       1423 TCCAATGGGAAGTGCCTCTCGAAAAGCCAGCAGTGCAATGGGAAGGACGACTGTGGGGAC 1482

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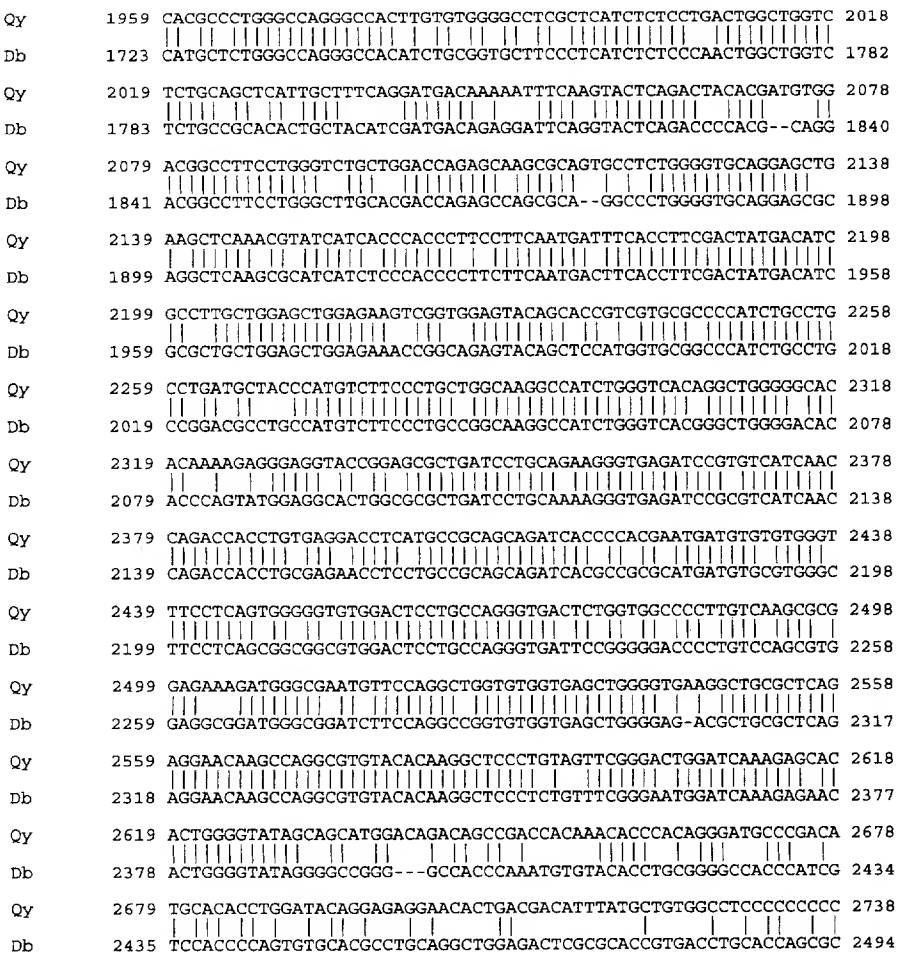
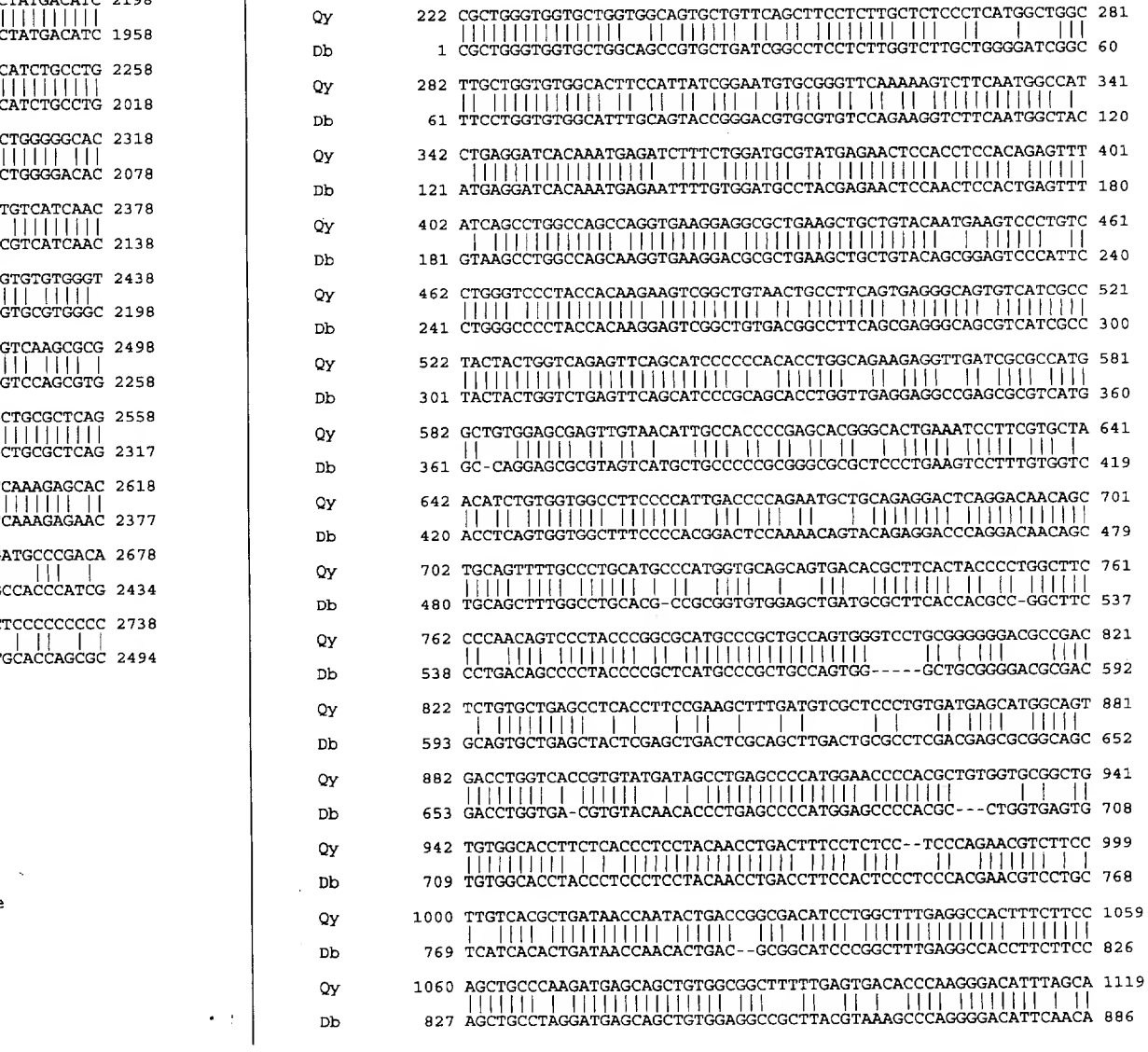


RESULT 5
US-09-644-600-9
; Sequence 9, Application US/09644600
; Patent No. 6451500
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotoshi
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
; TITLE OF INVENTION: Overexpressed in Carcinomas
; FILE REFERENCE: D6064CIP/D
; CURRENT APPLICATION NUMBER: US/09/644,600
; CURRENT FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/421,213
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: 09/027,337
; PRIOR FILING DATE: 1998-02-20

; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 9
; LENGTH: 2900
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: SNC-19; GeneBank Accession No. 6451500 #U20428
US-09-644-600-9

Query Match 49.3%; Score 1530.8; DB 4; Length 2900;
Best Local Similarity 79.1%; Pred. No. 0;
Matches 2011; Conservative 0; Mismatches 502; Indels 29; Gaps 15;



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Db       1306 AGTTCACGTGCAAGAGCAAGTTCTGCAAG---CTCTTCTGGGTCTGCGACAGTGTGAACG 1362
Qy       1600 ACTGTGGGGACGGAAGTGACGAGGAGGGCTGCAGCTGTCCTG-CTGGGAGTTTCAAGTGT 1658
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Qy       1719 GGGTCTGACGAGGCTTCATGTGACAGCGTGAATGTCGTCTCTTGCACCAAATATACCTAC 1778
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Qy       1779 CGCTGCCAAAATGGCCTCTGTCTGAGCAAGGGCAACCCTGAGTGTGATGGGAAGACGGAC 1838
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Db       1841 ACGGCCTTCCTGGGCTTGCACGACCAGAGCCAGCGCA--GGCCCTGGGGTGCAGGAGCGC 1898
Qy       2139 AAGCTCAAACGTATCATCACCCACCCTTCCTTCAATGATTTCACCTTCGACTATGACATC 2198
Db       1899 AGGCTCAAGCGCATCATCTCCCACCCCTTCTTCAATGACTTCACCTTCGACTATGACATC 1958
Qy       2199 GCCTTGCTGGAGCTGGAGAAGTCGGTGGAGTACAGCACCGTCGTGCGCCCCATCTGCCTG 2258
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Qy       2259 CCTGATGCTACCCATGTCTTCCCTGCTGGCAAGGCCATCTGGGTCACAGGCTGGGGGCAC 2318
Db       2019 CCGGACGCCTGCCATGTCTTCCCTGCCGGCAAGGCCATCTGGGTCACGGGCTGGGGACAC 2078
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Db       2139 CAGACCACCTGCGAGAACCTCCTGCCGCAGCAGATCACGCCGCGCATGATGTGCGTGGGC 2198
Qy       2439 TTCCTCAGTGGGGGTGTGGACTCCTGCCAGGGTGACTCTGGTGGCCCCTTGTCAAGCGCG 2498
Db       2199 TTCCTCAGCGGCGGCGTGGACTCCTGCCAGGGTGATTCCGGGGGACCCCTGTCCAGCGTG 2258
Qy       2499 GAGAAAGATGGGCGAATGTTCCAGGCTGGTGTGGTGAGCTGGGGTGAAGGCTGCGCTCAG 2558
Db       2259 GAGGCGGATGGGCGGATCTTCCAGGCCGGTGTGGTGAGCTGGGGAG-ACGCTGCGCTCAG 2317
Qy       2559 AGGAACAAGCCAGGCGTGTACACAAGGCTCCCTGTAGTTCGGGACTGGATCAAAGAGCAC 2618
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Qy       2619 ACTGGGGTATAGCAGCATGGACAGACAGCCGACCACAAACACCCACAGGGATGCCCGACA 2678
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RESULT 6
US-09-280-116-10
; Sequence 10, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1553
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: trypsin-like serine proteases
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1553)
; OTHER INFORMATION: n = a, t, c, or g
US-09-280-116-10

Query Match 22.6%; Score 701.2; DB 4; Length 1553;
Best Local Similarity 71.1%; Pred. No. 1.2e-177;
Matches 1092; Conservative 0; Mismatches 351; Indels 92; Gaps 9;

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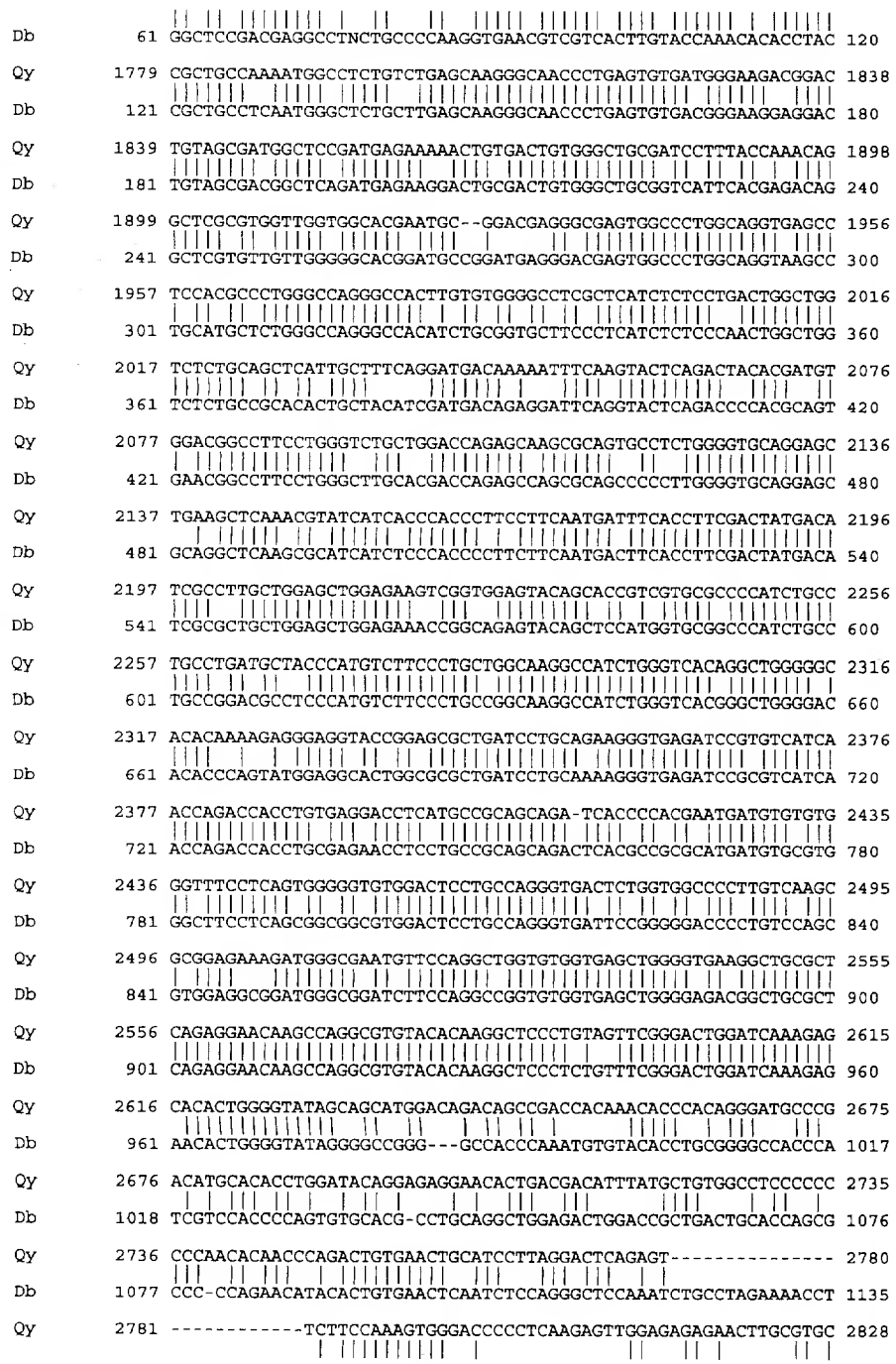

RESULT 7
US-09-702-705-1480
; Sequence 1480, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1480
; LENGTH: 434
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-702-705-1480

Query Match 9.9%; Score 306.8; DB 4; Length 434;
Best Local Similarity 82.1%; Pred. No. 2e-72;
Matches 353; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

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Qy       1503 AGTGATGAGC 1512
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Db        421 AGCGATGAGC 430
```

RESULT 8
US-09-736-457-1480
; Sequence 1480, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1480
; LENGTH: 434
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-736-457-1480

Query Match 9.9%; Score 306.8; DB 4; Length 434;
Best Local Similarity 82.1%; Pred. No. 2e-72;
Matches 353; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

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Qy       1083 GGCGGCTTTTTGAGTGACACCCAAGGGACATTTAGCAGCCCCTACTATCCAGGCCACTAC 1142
             || |||   ||  || |  |||| |||||||| | |||||||||||| ||||||||||||
Db          1 GGAGGCCGCTTACGTAAAGCCCAGGGGACATTCAACAGCCCCTACTACCCAGGCCACTAC 60

Qy       1143 CCGCCCAACATCAACTGCACATGGAATATCAAGGTGCCCAACAACCGGAACGTGAAGGTG 1202
             || |||||||  |||||||||||||| ||  |||||||||||||||| | | |||||||||
Db         61 CCACCCAACATTGACTGCACATGGAACATTGAGGTGCCCAACAACCAGCATGTGAAGGTG 120

Qy       1203 CGCTTCAAACTCTTCTATCTGGTGGACCCCAACGTACCAGTGGGCTCCTGCACCAAGGAC 1262
             |||||||| ||||||| ||| |||| |||  ||| || | |||| |||| ||||||||
Db        121 CGCTTCAAATTCTTCTACCTGCTGGAGCCCGGCGTGCCTGCGGGCACCTGCCCCAAGGAC 180

Qy       1263 TATGTGGAGATCAACGGGGAGAAGTACTGCGGTGAGAGGTCCCAGTTTGTGGTGAGCAGC 1322
             || |||||||||| |||||||| |||||||| |||||||||||||| || || | ||||
Db        181 TACGTGGAGATCAATGGGGAGAAATACTGCGGAGAGAGGTCCCAGTTCGTCGTCACCAGC 240

Qy       1323 AACAGCAGCAAGATTACAGTCCACTTCCATTCTGATCACTCGTACACGGACACCGGGTTC 1382
             ||||||| ||||||| ||||| | |||||| || ||||| || ||||| |||||||| |||
Db        241 AACAGCAACAAGATCACAGTTCGCTTCCACTCAGATCAGTCCTACACCGACACCGGCTTC 300

Qy       1383 CTAGCTGAGTACCTCTCCTACGACTCCAACGACCCGTGCCCAGGGATGTTCATGTGCAAG 1442
             |||||||||||||||||||||||  ||||| ||||| |||  ||||| ||||
Db        301 TTAGCTGAATACCTCTCCTACGACTCCAGTGACCCATGCCCGGGGCAGTTCACGTGCCGC 360

Qy       1443 ACTGGACGGTGCATCCGAAAGGAACTGCGCTGCGACGGCTGGGCAGACTGCCCGGATTAT 1502
             || || ||||| ||||| ||||| |||||||| || |||||||| |||||| | ||  |
Db        361 ACGGGGCGGTGTATCCGGAAGGAGCTGCGCTGTGATGGCTGGGCCGACTGCACCGACCAC 420

Qy       1503 AGTGATGAGC 1512
             || |||||||
Db        421 AGCGATGAGC 430
```

RESULT 9
US-09-280-116-107
; Sequence 107, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 107
; LENGTH: 796
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: trypsin-like serine proteases
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(796)
; OTHER INFORMATION: n = a, t, c or g
US-09-280-116-107

Query Match 5.6%; Score 173.2; DB 4; Length 796;
Best Local Similarity 57.7%; Pred. No. 1.4e-36;
Matches 395; Conservative 0; Mismatches 269; Indels 21; Gaps 4;

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Qy       1744 GCGTGAATGTCGTCTCTTGCACCAAATATACCTACCGCTGCCAAAATGGCCTCTGTCTGA 1803
             ||  | | |  ||  | ||   | ||  |||| ||  ||  | | |  |||  |||
Db         106 GCCAGGAAGGGGTGCCATGTGGGACATTCACCTTCCAGTGTGAGGACCGGAGCTGCGTGA 165

Qy       1804 GCAAGGGCAACCCTGAGTGTGATGGGAAGACGGACTGTAGCGATGGCTCCGATGAGAAAA 1863
             |||  ||||||  |||||||||||  | | ||||| || || |||||  ||||||  |
Db         166 AGAAGCCCAACCCGCAGTGTGATGGGCGGCCCGACTGCAGGGACGGCTCGGATGAGGAGC 225

Qy       1864 ACTGTGACTGTGGGCTGCGATCCTTTACCAAACAGGCTCGCGTGGTTGGTGGCACGAATG 1923
             |||||||||||||| || |    |  |||         ||| | ||||||||  |
Db         226 ACTGTGACTGTGGCCTCCAGGGCCCCTCCA------GCCGCATTGTTGGTGGAGCTGTGT 279

Qy       1924 CGGACGAGGGCGAGTGGCCCTGGCAGGTGAGCCTCCACGCCCTGGGCCAGGGCCACTTGT 1983
             |   ||||||  |||||||| |||||||  ||||||||  |  | |||  |   | |||  | |
Db         280 CCTCCGAGGGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTCGGGGTC---GACACATCT 336

Qy       1984 GTGGGGCCTCGCTCATCTCTCCTGACTGGCTGGTCTCTGCAGCTCATTGCTTTCAGGATG 2043
             ||||||   | ||||||  ||     |||| ||  |  | ||  ||  || ||||| ||||| |
Db         337 GTGGGGGGGCCCTCATCGCTGACCGCTGGGTGATAACAGCTGCCCACTGCTTCCAGGAGG 396

Qy       2044 ACAAAAATTTCAAGTACTCAGACTACACGATGTGGACGGCCTTCCTGGGTCTGCTGGACC 2103
             |||  |          |   |     | |||||||  |  ||||||||   | ||   |
Db         397 ACAGCA---------TGGCCTCCACGGTGCTGTGGACCGTGTTCCTGGGCAAGGTGTGGC 447

Qy       2104 AGAGCAAGCGCAGTGCCTCTGGGGTGCAGGAGCTGAAGCTCAAACGTATCATCACCCACC 2163
             |||  |  ||||  |     ||||  | |   |     | |||  |  |  ||  |  ||||
Db         448 AGAACTCGCGCTG---GCCTGGAGAGGTGTCCTTCAAGGTGAGCCGCCTGCTCCTGCACC 504

Qy       2164 CTTCCTTCAATGATTTCACCTTCGACTATGACATCGCCTTGCTGGAGCTGGAGAAGTCGG 2223
             | | |  | | ||   || |   |||||  |||  | ||  |||||  ||||  ||   |  |||
Db         505 CGTACCACGAAGAGGACAGCCATGACTACGACGTGGCGCTGCTGCAGCTCGACCACCCGG 564

Qy       2224 TGGAGTACAGCACCGTCGTGCGCCCCATCTGCCTGCCTGATGCTACCCATGTCTTCCCTG 2283
             |||  |   |||  |||||||||| |||||||||| |       ||||  |||||
Db         565 TGGTGCGCTCGGCCGCCGTGCGCCCCGTCTGCCTGCCCGCGCGCTCCCACTTCTTCGAGC 624
```

```
Qy       2284 CTGGCAAGGCCATCTGGGTCACAGGCTGGGGGCACACAAAAGAGGGAGGTACCGGAGCGC 2343
Db        625 CCGGCCTGCACTGCTGGATTACGGGCTGGGGCGCCTTGCGCGAGGGCGGCCCCATCAGCA 684

Qy       2344 TGATCCTGCAGAAGGGTGAGATCCGTGTCATCAACCAGACCACCTGTGAGGACCTCATGC 2403
Db        685 ACGCTCTGCAGAAAGTGGATGTGCANTTGATCCCACAGGACCTGTGCAGCGAGGTCTATC 744

Qy       2404 CGCAGCAGATCACCCCACGAATGAT 2428
Db        745 GCTACCAGGTGACGCCACGCATGCT 769
```

RESULT 10
US-09-518-046-1
; Sequence 1, Application US/09518046
; Patent No. 6294663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; TITLE OF INVENTION: in Ovarian Carcinoma and Uses Thereof
; FILE REFERENCE: D6192CIP
; CURRENT APPLICATION NUMBER: US/09/518,046
; CURRENT FILING DATE: 2000-03-02
; EARLIER APPLICATION NUMBER: 09/261,416
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 1
; LENGTH: 2413
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; OTHER INFORMATION: entire cDNA sequence of TADG-12 gene
US-09-518-046-1

Query Match 3.7%; Score 113.6; DB 3; Length 2413;
Best Local Similarity 52.6%; Pred. No. 2.1e-20;
Matches 388; Conservative 0; Mismatches 314; Indels 36; Gaps 5;

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Qy       1900 CTCGCGTGGTTGGTGGCACGAATGCGGACGAGGGCGAGTGGCCCTGGCAGGTGAGCCTCC 1959
Db        790 CACGCATCGTGGGTGGAAACATGTCCTTGCTCTCGCAGTGGCCCTGGCAGGCCAGCCTTC 849

Qy       1960 ACGCCCTGGGCCAGGGCCACTTGTGTGGGGCCTCGCTCATCTCTCCTGACTGGCTGGTCT 2019
Db        850 AGTTCCAGGGCTA---CCACCTGTGCGGGGGCTCTGTCATCACGCCCCTGTGGATCATCA 906

Qy       2020 CTGCAGCTCATTGCTTTCAGGATGACAAAAATTTCAAGTACTCAGACTACACGATGTGGA 2079
Db        907 CTGCTGCACACTGTGTTTATGACTTGTACCTCCCCAAGTCATGGACCATCCAGGTGGGTC 966

Qy       2080 CGGCCTTCCTGGGTCTGCTGGACCAGAGCAAGCGCAGTGCCTCTGGGGTGCAGGAGCTGA 2139
Db        967 TAGTTTCCCTG-------TTGGACAATCCAGCCCCATCCCACTTGGTGGAGAAG------ 1013

Qy       2140 AGCTCAAACGTATCATCACCCACCCTTCCTTCAATGATTTCACCTTCGACTATGACATCG 2199
Db       1014 -----------ATTGTCTACCACAGCAAGTACAAGCCAAAGAGGCTGGGCAATGACATCG 1062

Qy       2200 CCTTGCTGGAGCTGGAGAAGTCGGTGGAGTACAGCACCGTCGTGCGCCCCATCTGCCTGC 2259
Db       1063 CCCTTATGAAGCTGGCCGGGCCACTCACGTTCAATGAAATGATCCAGCCTGTGTGCCTGC 1122

Qy       2260 CTGATGCTACCCATGTCTTCCCTGCTGGCAAGGCCATCTGGGTCACAGGCTGGGGGCACA 2319
Db       1123 CCAACTCTGAAGAGAACTTCCCCGATGGAAAAGTGTGCTGGACGTCAGGATGGGGGGCCA 1182

Qy       2320 CAAAAGAGGGAGGTACCGGAGCGCTGATCCTGCAGAAGGGTGAGATCCGTGTCATCAACC 2379
Db       1183 CAGAGGATGGAGGTGACGCCTCCCCTGTCCTGAACCACGCGGCCGTCCCTTTGATTTCCA 1242

Qy       2380 AGACCACCTGTGA------GGACCTCATGCCGCAGCAGATCACCCCACGAATGATGTGTG 2433
Db       1243 ACAAGATCTGCAACCACAGGGACGTGTACGGTGGCATCATCTCCCCCTCCATGCTCTGCG 1302

Qy       2434 TGGGTTTCCTCAGTGGGGGTGTGGACTCCTGCCAGGGTGACTCTGGTGGCCCCTTGTCAA 2493
Db       1303 CGGGCTACCTGACGGGTGGCGTGAACAGCTGCCAGGGGGACAGCGGGGGGCCCCTGGTGT 1362

Qy       2494 GCGCGGAGAAAGATGGGCGAATGTTCCAGGCTGGTGTGGTGAGCTGGGGTGAAGGCTGCG 2553
Db       1363 GTCAAGAGAGGAGGCTGTGGAAGTT---AGTGGGAGCGACCAGCTTTGGCATCGGCTGCG 1419

Qy       2554 CTCAGAGGAACAAGCCAGGCGTGTACACAAGGCTCCCTGTAGTTCGGGACTGGATCAAAG 2613
Db       1420 CAGAGGTGAACAAGCCTGGGGTGTACACCCGTGTCACCTCCTTCCTGGACTGGATCCACG 1479

Qy       2614 AGCACACTGGGGTATAGC 2631
Db       1480 AGCAGATGGAGAGAGACC 1497

RESULT 11
US-09-518-046-3
; Sequence 3, Application US/09518046
; Patent No. 6294663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; TITLE OF INVENTION: in Ovarian Carcinoma and Uses Thereof
; FILE REFERENCE: D6192CIP
; CURRENT APPLICATION NUMBER: US/09/518,046
; CURRENT FILING DATE: 2000-03-02
; EARLIER APPLICATION NUMBER: 09/261,416
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 3
; LENGTH: 2544
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; OTHER INFORMATION: entire cDNA sequence of TADG-12 variant gene
US-09-518-046-3

Query Match 3.5%; Score 109.8; DB 3; Length 2544;
Best Local Similarity 54.6%; Pred. No. 2.3e-19;
Matches 266; Conservative 0; Mismatches 212; Indels 9; Gaps 2;

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Qy   2151 ATCATCACCCACCCTTCCTTCAATGATTTCACCTTCGACTATGACATCGCCTTGCTGGAG 2210
Db   1145 ATTGTCTACCACAGCAAGTACAAGCCAAAGAGGCTGGGCAATGACATCGCCCTTATGAAG 1204

Qy   2211 CTGGAGAAGTCGGTGGAGTACAGCACCGTCGTGCGCCCCATCTGCCTGCCTGATGCTACC 2270
Db   1205 CTGGCCGGGCCACTCACGTTCAATGAAATGATCCAGCCTGTGTGCCTGCCCAACTCTGAA 1264

Qy   2271 CATGTCTTCCCTGCTGGCAAGGCCATCTGGGTCACAGGCTGGGGGCACACAAAAGAGGGA 2330
Db   1265 GAGAACTTCCCCGATGGAAAAGTGTGCTGGACGTCAGGATGGGGGGCCACAGAGGATGGA 1324

Qy   2331 GGTACCGGAGCGCTGATCCTGCAGAAGGGTGAGATCCGTGTCATCAACCAGACCACCTGT 2390
Db   1325 GGTGACGCCTCCCCTGTCCTGAACCACGCGGCCGTCCCTTTGATTTCCAACAAGATCTGC 1384

Qy   2391 GA------GGACCTCATGCCGCAGCAGATCACCCCACGAATGATGTGTGTGGGTTTCCTC 2444
Db   1385 AACCACAGGGACGTGTACGGTGGCATCATCTCCCCCTCCATGCTCTGCGCGGGCTACCTG 1444

Qy   2445 AGTGGGGGTGTGGACTCCTGCCAGGGTGACTCTGGTGGCCCCTTGTCAAGCGCGGAGAAA 2504
Db   1445 ACGGGTGGCGTGGACAGCTGCCAGGGGGACAGCGGGGGGCCCCTGGTGTGTCAAGAGAGG 1504
```
```

```
Qy       2505 GATGGGCGAATGTTCCAGGCTGGTGTGGTGAGCTGGGGTGAAGGCTGCGCTCAGAGGAAC 2564
Db       1505 AGGCTGTGGAAGTT---AGTGGGAGCGACCAGCTTTGGCATCGGCTGCGCAGAGGTGAAC 1561

Qy       2565 AAGCCAGGCGTGTACACAAGGCTCCCTGTAGTTCGGGACTGGATCAAAGAGCACACTGGG 2624
Db       1562 AAGCCTGGGGTGTACACCCGTGTCACCTCCTTCCTGGACTGGATCCACGAGCAGATGGAG 1621

Qy       2625 GTATAGC 2631
Db       1622 AGAGACC 1628


RESULT 12
US-09-342-749-1
; Sequence 1, Application US/09342749
; Patent No. 6166194
; GENERAL INFORMATION:
;  APPLICANT: Wong, Alexander K.C.
;  APPLICANT: Tavtigian, Sean V.
;  APPLICANT: Teng, DAvid H.-F.
;  APPLICANT: Myriad Genetics, Inc.
;  TITLE OF INVENTION: TMPRSS2 is a Tumor Suppressor
;  FILE REFERENCE: 2318-202
;  CURRENT APPLICATION NUMBER: US/09/342,749
;  CURRENT FILING DATE: 1999-06-29
;  EARLIER APPLICATION NUMBER: US 60/091,044
;  EARLIER FILING DATE: 1998-06-29
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 1479
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1476)
;   FEATURE:
;   NAME/KEY: conflict
;   LOCATION: (724)
;   OTHER INFORMATION: Listed as T in GenBank Accession NO. U75329
;   FEATURE:
;   NAME/KEY: conflict
;   LOCATION: (985)
;   OTHER INFORMATION: Listed as C in GenBank Accession No. 6166194 U75329
;   FEATURE:
;   NAME/KEY: conflict
;   LOCATION: (1347)
;   OTHER INFORMATION: Listed as C in GenBank Accession No. 6166194 U75329
;   FEATURE:
;   NAME/KEY: conflict
;   LOCATION: (1466)
;   OTHER INFORMATION: Listed as A in GenBank Accession No. 6166194 U75329
;   FEATURE:
;   NAME/KEY: conflict
;   LOCATION: (1471)
;   OTHER INFORMATION: Listed as A in GenBank Accession No. 6166194 U75329.
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: (478)
;   OTHER INFORMATION: This base can be G or A with G being the more
;   OTHER INFORMATION: common allele. The codon will change from Val to
;   OTHER INFORMATION: Met.
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: (777)
;   OTHER INFORMATION: This base can be C or T with C being the more
;   OTHER INFORMATION: common allele.  The codon is unaffected with both
;   OTHER INFORMATION: alleles encoding Gly.
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: (768)
;   OTHER INFORMATION: This base can be C or T with C being the more
;   OTHER INFORMATION: common allele.  This is a silent polymorphism.
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: (834)
;   OTHER INFORMATION: This base can be C or T with C being the more
;   OTHER INFORMATION: common allele.  This is a silent polymorphism.
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: (625)
;   OTHER INFORMATION: This base can be T or A with T being the more
;   OTHER INFORMATION: common allele.  The codon will change from Phe to
;   OTHER INFORMATION: Ile
US-09-342-749-1

  Query Match             3.3%;  Score 101.6;  DB 3;  Length 1479;
  Best Local Similarity   52.8%;  Pred. No. 2.7e-17;
  Matches  396;  Conservative    0;  Mismatches  324;  Indels   30;  Gaps    7;

Qy       1886 CTTTACCAAACAGGCTCGCGTGGTTGGTGGCACGAATGCGGACGAGGGCGAGTGGCCCTG 1945
Db        747 CTCAAGCCGCCAGAGCAGGATCGTGGGCGGCGAGAGCGCGCTCCCGGGGGCCTGGCCCTG 806

Qy       1946 GCAGGTGAGCCTCCACGCCCTGGGCCAGGGCCACTTGTGTGGGGCCTCGCTCATCTCTCC 2005
Db        807 GCAGGTCAGCCTGCACGTCCAGAAC---GTCCACGTGTGCGGAGGCTCCATCATCACCCC 863

Qy       2006 TGACTGGCTGGTCTCTGCAGCTCATTGCTTTCAGGATGACAAAAATTTCAAGTACTCAGA 2065
Db        864 CGAGTGGATCGTGACAGCCGCCCACTGC------GTGGAAAAACCTCTTAACAATCCATG 917

Qy       2066 CTACACGATGTGGACGGCCTTCCTGGGTCTGCTGGACCAGAGCAAGCGCAGTGCCTCTGG 2125
Db        918 GCAT------TGGACGGCATTTGCGGGGATTTTGAGA-----CAATCTTTCATGTTCTAT 966

Qy       2126 GGTGCAGGAGCTGAAGCTCAAACGTATCATCACCCACCCTTCCTTCAATGATTTCACCTT 2185
Db        967 GGAGCCGGATACCAAG-TAGAAAAAGTGATTTCTCATCCAAATTATGACTCCAAGACCAA 1025

Qy       2186 CGACTATGACATCGCCTTGCTGGAGCTGGAGAAGTCGGTGGAGTACAGCACCGTCGTGCG 2245
Db        1026 GAACAATGACATTGCGCTGATGAAGCTGCAGAAGCCTCTGACTTTCAACGACCTAGTGAA 1085

Qy       2246 CCCCATCTGCCTGCCTGATGCTACCCATGTCTTCCCTGCTGGCAAGGCCATCTGGGTCAC 2305
Db        1086 ACCAGTGTGTCTGCCCAACCCAGGCATGATGCTGCAGCCAGAACAGCTCTGCTGGATTTC 1145

Qy       2306 AGGCTGGGGGCACACAAAAGAGGGAGGTA------CCGGAGCGCTGATCCTGCAGAAGGG 2359
Db        1146 CGGGTGGGGGGCCACCGAGGAGAAAGGGAAGACCTCAGAAGTGCTGAACGCTGCCAAGGT 1205

Qy       2360 TGAGATCCGTGTCATCAACCAGACCACCTGTGAGGACCTCATGCCGCAGCAGATCACCCC 2419
Db        1206 GCTTCTCATTGAGACACAGAGATGCAACAGCAGATATGTCTATGACAACCTGATCACACC 1265

Qy       2420 ACGAATGATGTGTGTGGGTTTCCTCAGTGGGGGTGTGGACTCCTGCCAGGGTGACTCTGG 2479
Db        1266 AGCCATGATCTGTGCCGGCTTCCTGCAGGGGAACGTCGATTCTTGCCAGGGTGACAGTGG 1325

Qy       2480 TGGCCCCTTGTCAAGCGCGGAGAAAGATGGGCGAATGTTCCAGGCTGGTGTGGTGAGCTG 2539
Db        1326 AGGGCCTCTGGTCACTTCGAAGAACAATATCTG---GTGGCTGATAGGGGATACAAGCTG 1382

Qy       2540 GGGTGAAGGCTGCGCTCAGAGGAACAAGCCAGGCGTGTACACAAGGCTCCCTGTAGTTCG 2599
Db        1383 GGGTTCTGGCTGTGCCAAAGCTTACAGACCAGGAGTGTACGGGAATGTGATGGTATTCAC 1442

Qy       2600 GGACTGGATCAAAGAGCACACTGGGGTATA 2629
Db        1443 GGACTGGATTTATCGACAAATGAGGGCAGA 1472


RESULT 13
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```
US-09-691-840-1
; Sequence 1, Application US/09691840
; Patent No. 6444419
; GENERAL INFORMATION:
;  APPLICANT: Wong, Alexander K.C.
;  APPLICANT:  Tavtigian, Sean V.
;  APPLICANT:  Teng, DAvid H.-F.
;  APPLICANT:  Myriad Genetics, Inc.
;  TITLE OF INVENTION: TMPRSS2 is a Tumor Suppressor
;  FILE REFERENCE: 2318-202
;  CURRENT APPLICATION NUMBER: US/09/691,840
;  CURRENT FILING DATE:  2000-10-18
;  PRIOR APPLICATION NUMBER: US/09/342,749
;  PRIOR FILING DATE: 1999-06-29
;  PRIOR APPLICATION NUMBER: US 60/091,044
;  PRIOR FILING DATE: 1998-06-29
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 1479
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1476)
;   NAME/KEY: conflict
;   LOCATION: (724)
;   OTHER INFORMATION: Listed as T in GenBank Accession NO. U75329
;   NAME/KEY: conflict
;   LOCATION: (985)
;   OTHER INFORMATION: Listed as C in GenBank Accession No. 6444419 U75329
;   NAME/KEY: conflict
;   LOCATION: (1347)
;   OTHER INFORMATION: Listed as C in GenBank Accession No. 6444419 U75329
;   NAME/KEY: conflict
;   LOCATION: (1466)
;   OTHER INFORMATION: Listed as A in GenBank Accession No. 6444419 U75329
;   NAME/KEY: conflict
;   LOCATION: (1471)
;   OTHER INFORMATION: Listed as A in GenBank Accession No. 6444419 U75329.
;   NAME/KEY: allele
;   LOCATION: (478)
;   OTHER INFORMATION: This base can be G or A with G being the more
;   OTHER INFORMATION: common allele. The codon will change from Val to
;   OTHER INFORMATION: Met.
;   NAME/KEY: allele
;   LOCATION: (777)
;   OTHER INFORMATION: This base can be C or T with C being the more
;   OTHER INFORMATION: common allele.  The codon is unaffected with both
;   OTHER INFORMATION: alleles encoding Gly.
;   NAME/KEY: allele
;   LOCATION: (768)
;   OTHER INFORMATION: This base can be C or T with C being the more
;   OTHER INFORMATION: common allele.  This is a silent polymorphism.
;   NAME/KEY: allele
;   LOCATION: (834)
;   OTHER INFORMATION: This base can be C or T with C being the more
;   OTHER INFORMATION: common allele.  This is a silent polymorphism.
;   NAME/KEY: allele
;   LOCATION: (625)
;   OTHER INFORMATION: This base can be T or A with T being the more
;   OTHER INFORMATION: common allele.  The codon will change from Phe to Ile
US-09-691-840-1

  Query Match             3.3%;  Score 101.6;  DB 4;  Length 1479;
  Best Local Similarity   52.8%;  Pred. No. 2.7e-17;
  Matches  396;  Conservative    0;  Mismatches  324;  Indels   30;  Gaps    7;

Qy       1886 CTTTACCAAACAGGCTCGCGTGGTTGGTGGCACGAATGCGGACGAGGGCGAGTGGCCCTG 1945
              ||  | |   |||     |  | || || |||  ||  |||  |  |||  |  ||||||||
Db        747 CTCAAGCCGCCAGAGCAGGATCGTGGGCGGCGAGAGCGCGCTCCCGGGGGCCTGGCCCTG 806

Qy       1946 GCAGGTGAGCCTCCACGCCCTGGGCCAGGGCCACTTGTGTGGGGCCTCGCTCATCTCTCC 2005
              ||||||  |||||  ||||  ||  |  |    |  ||||  ||||  ||  |  |||  |||||  |  ||
Db        807 GCAGGTCAGCCTGCACGTCCAGAAC---GTCCACGTGTGCGGAGGCTCCATCATCACCCC 863

Qy       2006 TGACTGGCTGGTCTCTGCAGCTCATTGCTTTCAGGATGACAAAAATTTCAAGTACTCAGA 2065
              ||  |||  |  ||   |  ||  ||  ||  |||       |   ||  |||   |  |  ||   |   ||
Db        864 CGAGTGGATCGTGACAGCCGCCCACTGC------GTGGAAAAACCTCTTAACAATCCATG 917

Qy       2066 CTACACGATGTGGACGGCCTTCCTGGGTCTGCTGGACCAGAGCAAGCGCAGTGCCTCTGG 2125
              |       |||||||| ||    |||   |  ||          |||  |          |||
Db        918 GCAT------TGGACGGCATTTGCGGGGATTTTGAGA-----CAATCTTTCATGTTCTAT 966

Qy       2126 GGTGCAGGAGCTGAAGCTCAAACGTATCATCACCCACCCTTCCTTCAATGATTTCACCTT 2185
              ||  ||  |||     |||  |   ||      |  ||   |  ||  ||    |    |         |||
Db        967 GGAGCCGGATACCAAG-TAGAAAAAGTGATTTCTCATCCAAATTATGACTCCAAGACCAA 1025

Qy       2186 CGACTATGACATCGCCTTGCTGGAGCTGGAGAAGTCGGTGGAGTACAGCACCGTCGTGCG 2245
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Db       1026 GAACAATGACATTGCGCTGATGAAGCTGCAGAAGCCTCTGACTTTCAACGACCTAGTGAA 1085

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              ||  |  ||  ||||||  |   |   |     |  |  |   |  |   ||  |  ||||  |  |
Db       1086 ACCAGTGTGTCTGCCCAACCCAGGCATGATGCTGCAGCCAGAACAGCTCTGCTGGATTTC 1145

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Qy       2360 TGAGATCCGTGTCATCAACCAGACCACCTGTGAGGACCTCATGCCGCAGCAGATCACCCC 2419
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RESULT 14
US-09-016-366A-20
; Sequence 20, Application US/09016366A
; Patent No. 5955431
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, Richard L.
;    APPLICANT:  Huang, Chifu
;    TITLE OF INVENTION:  MAST CELL PROTEASE PEPTIDE
;    TITLE OF INVENTION:  INHIBITORS
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/016,366A
;      FILING DATE:  January 30, 1998
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;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/037,090
;      FILING DATE:  05-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plumer, Elizabeth R.
;      REGISTRATION NUMBER:  36,637
;      REFERENCE/DOCKET NUMBER:  B0801/7093
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1128 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-016-366A-20

  Query Match             3.3%;  Score 101.2;  DB 2;  Length 1128;
  Best Local Similarity   53.1%;  Pred. No. 3.1e-17;
  Matches  394;  Conservative    0;  Mismatches  288;  Indels   60;  Gaps    6;

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Db         87 GCATCGTTGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 146

Qy       1957 TCCACGCCCTGGGCCAGGGCCACTTGTGTGGGGCCTCGCTCATCTCTCCTGACTGGCTGG 2016
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Qy       2137 TGAAGCTCAAACGTATCATCACCCACCCTTCCTTCAATGATTTCACCTTCGACTATGACA 2196
Db        303 TGCCGGTCAGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACA 362

Qy       2197 TCGCCTTGCTGGAGCTGGAGAAGTCGGTGGAGTACAGCACCGTCGTGCGCCCCATCTGCC 2256
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Qy       2257 TGCCTGATGCTACCCATGTCTTCCCTGCTGGCAAGGCCATCTGGGTCACAGGCTGGGG-- 2314
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Qy       2315 ----GCACACAAAAGAGGGAGGTACCGGAGCGCTGATCCTGCAGAAGGGTGAGATCCGTG 2370
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Qy       2530 TGGTGAGCTGGGGTGAAGGCTGCGCTCAGAGGAACAAGCCAGGCGTGTACACAAGGCTCC 2589
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; Sequence 15, Application US/08978404B
; Patent No. 5968782
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, Richard L.
;    TITLE OF INVENTION:  MAST CELL PROTEASE THAT CLEAVES
;    TITLE OF INVENTION:  FIBRINOGEN
;    NUMBER OF SEQUENCES:  74
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/978,404B
;      FILING DATE:  25-NOV-97
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/032,354
;      FILING DATE:  04-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plumer, Elizabeth R.
;      REGISTRATION NUMBER:  36,637
;      REFERENCE/DOCKET NUMBER:  B0801/7090
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1128 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-978-404B-15

  Query Match             3.3%;  Score 101.2;  DB 2;  Length 1128;
  Best Local Similarity   53.1%;  Pred. No. 3.1e-17;
  Matches  394;  Conservative    0;  Mismatches  288;  Indels   60;  Gaps    6;

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Qy       1957 TCCACGCCCTGGGCCAGGGCCACTTGTGTGGGGCCTCGCTCATCTCTCCTGACTGGCTGG 2016
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Db        243 ATCTGGCCGCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGC 302

Qy       2137 TGAAGCTCAAACGTATCATCACCCACCCTTCCTTCAATGATTTCACCTTCGACTATGACA 2196
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Qy       2197 TCGCCTTGCTGGAGCTGGAGAAGTCGGTGGAGTACAGCACCGTCGTGCGCCCCATCTGCC 2256
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Qy       2257 TGCCTGATGCTACCCATGTCTTCCCTGCTGGCAAGGCCATCTGGGTCACAGGCTGGGG-- 2314
Db        423 TGCCCCCTGCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCG 482

Qy       2315 ----GCACACAAAAGAGGGAGGTACCGGAGCGCTGATCCTGCAGAAGGGTGAGATCCGTG 2370
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Qy       2371 TCATCAACCAGACCACCTGTGA----------------GGACCTCATGCCGCAGCAGATC 2414
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Qy       2530 TGGTGAGCTGGGGTGAAGGCTGCGCTCAGAGGAACAAGCCAGGCGTGTACACAAGGCTCC 2589
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Sequence: 1 catggtagacggctgcccgg.....ttaaaaaaaaaaaaaaaaaa 3106

Scoring table: IDENTITY_NUC
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Searched: 2449703 seqs, 1841816367 residues

Total number of hits satisfying chosen parameters: 4899406

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1883.2	60.6	3147	11	US-09-776-191-49	Sequence 49, Appl
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6	1883.2	60.6	3147	12	US-10-147-211A-3	Sequence 3, Appli
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20	1559.2	50.2	2756	9	US-09-925-301-351	Sequence 351, App
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39	239.2	7.7	1327	10	US-09-999-832A-170	Sequence 170, App
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43	239.2	7.7	1327	11	US-09-978-191A-170	Sequence 170, App
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; Sequence 1, Application US/09900751
; Patent No. US20020026653A1
; GENERAL INFORMATION:
;  APPLICANT: Allen, Keith D
;  APPLICANT:  Leviten, Michael W.
;  TITLE OF INVENTION: TRANSGENIC MICE CONTAINING SERINE
;  TITLE OF INVENTION:  PROTEASE GENE DISRUPTIONS
;  FILE REFERENCE: R-386
;  CURRENT APPLICATION NUMBER: US/09/900,751
;  CURRENT FILING DATE:  2001-07-06
;  PRIOR APPLICATION NUMBER: US 60/217,449
;  PRIOR FILING DATE: 2000-07-10
;  PRIOR APPLICATION NUMBER: US 60/223,170
;  PRIOR FILING DATE: 2000-08-07
;  PRIOR APPLICATION NUMBER: US 60/223,460
;  PRIOR FILING DATE: 2000-08-07
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 3106
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-900-751-1

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Qy         61 CCATGGGTAGCAATCGGGGCCGCAAGGCCGGAGGGGGCTCTCAGGACTTCGGCGCGGGAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      181 CTGCGAACAATGCCAAGAAAGTGGAGAAGCGAGGCCCCAGGCGCTGGGTGGTGCTGGTGG 240
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Qy      241 CAGTGCTGTTCAGCTTCCTCTTGCTCTCCCTCATGGCTGGCTTGCTGGTGTGGCACTTCC 300
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Qy      361 TCTTTCTGGATGCGTATGAGAACTCCACCTCCACAGAGTTTATCAGCCTGGCCAGCCAGG 420
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Qy     1141 ACCCGCCCAACATCAACTGCACATGGAATATCAAGGTGCCCAACAACCGGAACGTGAAGG 1200
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Qy     1261 ACTATGTGGAGATCAACGGGGAGAAGTACTGCGGTGAGAGGTCCCAGTTTGTGGTGAGCA 1320
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Qy     1321 GCAACAGCAGCAAGATTACAGTCCACTTCCATTCTGATCACTCGTACACGGACACCGGGT 1380
Db     1321 GCAACAGCAGCAAGATTACAGTCCACTTCCATTCTGATCACTCGTACACGGACACCGGGT 1380

Qy     1381 TCCTAGCTGAGTACCTCTCCTACGACTCCAACGACCCGTGCCCAGGGATGTTCATGTGCA 1440
Db     1381 TCCTAGCTGAGTACCTCTCCTACGACTCCAACGACCCGTGCCCAGGGATGTTCATGTGCA 1440

Qy     1441 AGACTGGACGGTGCATCCGAAAGGAACTGCGCTGCGACGGCTGGGCAGACTGCCCGGATT 1500
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Qy     1501 ATAGTGATGAGCGTTACTGCCGATGCAATGCCACCCACCAGTTCACGTGCAAAAACCAGT 1560
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Qy     1561 TCTGCAAGCCCCTCTTCTGGGTCTGTGACAGTGTCAACGACTGTGGGGACGGAAGTGACG 1620
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Qy     1621 AGGAGGGCTGCAGCTGTCCTGCTGGGAGTTTCAAGTGTTCCAATGGGAAGTGTCTCCCTC 1680
Db     1621 AGGAGGGCTGCAGCTGTCCTGCTGGGAGTTTCAAGTGTTCCAATGGGAAGTGTCTCCCTC 1680

Qy     1681 AGAGCCAGAAGTGTAATGGGAAGGACAACTGTGGAGATGGGTCTGACGAGGCTTCATGTG 1740
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Qy     1741 ACAGCGTGAATGTCGTCTCTTGCACCAAATATACCTACCGCTGCCAAAATGGCCTCTGTC 1800
Db     1741 ACAGCGTGAATGTCGTCTCTTGCACCAAATATACCTACCGCTGCCAAAATGGCCTCTGTC 1800

Qy     1801 TGAGCAAGGGCAACCCTGAGTGTGATGGGAAGACGGACTGTAGCGATGGCTCCGATGAGA 1860
Db     1801 TGAGCAAGGGCAACCCTGAGTGTGATGGGAAGACGGACTGTAGCGATGGCTCCGATGAGA 1860

Qy     1861 AAAACTGTGACTGTGGGCTGCGATCCTTTACCAAACAGGCTCGCGTGGTTGGTGGCACGA 1920
Db     1861 AAAACTGTGACTGTGGGCTGCGATCCTTTACCAAACAGGCTCGCGTGGTTGGTGGCACGA 1920

Qy     1921 ATGCGGACGAGGGCGAGTGGCCCTGGCAGGTGAGCCTCCACGCCCTGGGCCAGGGCCACT 1980
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Qy     1981 TGTGTGGGGCCTCGCTCATCTCTCCTGACTGGCTGGTCTCTGCAGCTCATTGCTTTCAGG 2040
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Qy     2041 ATGACAAAAATTTCAAGTACTCAGACTACACGATGTGGACGGCCTTCCTGGGTCTGCTGG 2100
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Qy     2101 ACCAGAGCAAGCGCAGTGCCTCTGGGGTGCAGGAGCTGAAGCTCAAACGTATCATCACCC 2160
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Qy     2161 ACCCTTCCTTCAATGATTTCACCTTCGACTATGACATCGCCTTGCTGGAGCTGGAGAAGT 2220
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Qy     2221 CGGTGGAGTACAGCACCGTCGTGCGCCCCATCTGCCTGCCTGATGCTACCCATGTCTTCC 2280
Db     2221 CGGTGGAGTACAGCACCGTCGTGCGCCCCATCTGCCTGCCTGATGCTACCCATGTCTTCC 2280

Qy     2281 CTGCTGGCAAGGCCATCTGGGTCACAGGCTGGGGGCACACAAAAGAGGGAGGTACCGGAG 2340
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Qy       2341 CGCTGATCCTGCAGAAGGGTGAGATCCGTGTCATCAACCAGACCACCTGTGAGGACCTCA 2400
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Db       2341 CGCTGATCCTGCAGAAGGGTGAGATCCGTGTCATCAACCAGACCACCTGTGAGGACCTCA 2400

Qy       2401 TGCCGCAGCAGATCACCCCACGAATGATGTGTGTGGGTTTCCTCAGTGGGGGTGTGGACT 2460
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Qy       2581 CAAGGCTCCCTGTAGTTCGGGACTGGATCAAAGAGCACACTGGGGTATAGCAGCATGGAC 2640
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Qy       2941 GGGAGCCCTATGGGAGGAGGGGCTCAGGGTCACTCTTTTCAGGAAGCGCCAGCCCTAGGA 3000
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Db       2941 GGGAGCCCTATGGGAGGAGGGGCTCAGGGTCACTCTTTTCAGGAAGCGCCAGCCCTAGGA 3000

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Db       3001 ACCCCAGAAAAGAGTGGTACCTAAGGCTGAAATTGTTTTGCTGTTGCCAGGGGTGGGTAT 3060

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; Sequence 968, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
;  APPLICANT: Afar, Daniel
;  APPLICANT:  Aziz, Natasha
;  APPLICANT:  Ginsberg, Wendy M.
;  APPLICANT:  Gish, Kurt C.
;  APPLICANT:  Glynne, Richard
;  APPLICANT:  Hevezi, Peter A.
;  APPLICANT:  Mack, David H.
;  APPLICANT:  Murray, Richard
;  APPLICANT:  Watson, Susan R.
;  APPLICANT:  Eos Biotechnology, Inc.
;  TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
;  TITLE OF INVENTION:  Methods of Screening for Modulators of Cancer
;  FILE REFERENCE: 018501-012500US
;  CURRENT APPLICATION NUMBER: US/10/295,027
;  CURRENT FILING DATE:  2002-11-13
;  PRIOR APPLICATION NUMBER: US 09/663,733
;  PRIOR FILING DATE: 2000-09-15
;  PRIOR APPLICATION NUMBER: US 60/350,666
;  PRIOR FILING DATE: 2001-11-13
;  PRIOR APPLICATION NUMBER: US 60/335,394
;  PRIOR FILING DATE: 2001-11-15
;  PRIOR APPLICATION NUMBER: US 60/332,464
;  PRIOR FILING DATE: 2001-11-21
;  PRIOR APPLICATION NUMBER: US 60/334,393
;  PRIOR FILING DATE: 2001-11-29
;  PRIOR APPLICATION NUMBER: US 60/340,376
;  PRIOR FILING DATE: 2001-12-14
;  PRIOR APPLICATION NUMBER: US 60/347,211
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: US 60/347,349
;  PRIOR FILING DATE: 2002-01-10
;  PRIOR APPLICATION NUMBER: US 60/355,250
;  PRIOR FILING DATE: 2002-02-08
;  PRIOR APPLICATION NUMBER: US 60/356,714
;  PRIOR FILING DATE: 2002-02-13
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1386
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 968
;   LENGTH: 3149
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-295-027-968

  Query Match            60.8%;  Score 1889.8;  DB 12;  Length 3149;
  Best Local Similarity  81.4%;  Pred. No. 0;
  Matches 2222;  Conservative    0;  Mismatches  504;  Indels    5;  Gaps    3;

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Db        263 GTGGCATTTGCAGTACCGGGACGTGCGTGTCCAGAAGGTCTTCAATGGCTACATGAGGAT 322

Qy        350 CACAAATGAGATCTTTCTGGATGCGTATGAGAACTCCACCTCCACAGAGTTTATCAGCCT 409
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Qy        410 GGCCAGCCAGGTGAAGGAGGCGCTGAAGCTGCTGTACAATGAAGTCCCTGTCCTGGGTCC 469
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Qy        470 CTACCACAAGAAGTCGGCTGTAACTGCCTTCAGTGAGGGCAGTGTCATCGCCTACTACTG 529
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Qy        530 GTCAGAGTTCAGCATCCCCCCACACCTGGCAGAAGAGGTTGATCGCGCCATGGCTGTGGA 589
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Qy        590 GCGAGTTGTAACATTGCCACCCCGAGCACGGGCACTGAAATCCTTCGTGCTAACATCTGT 649
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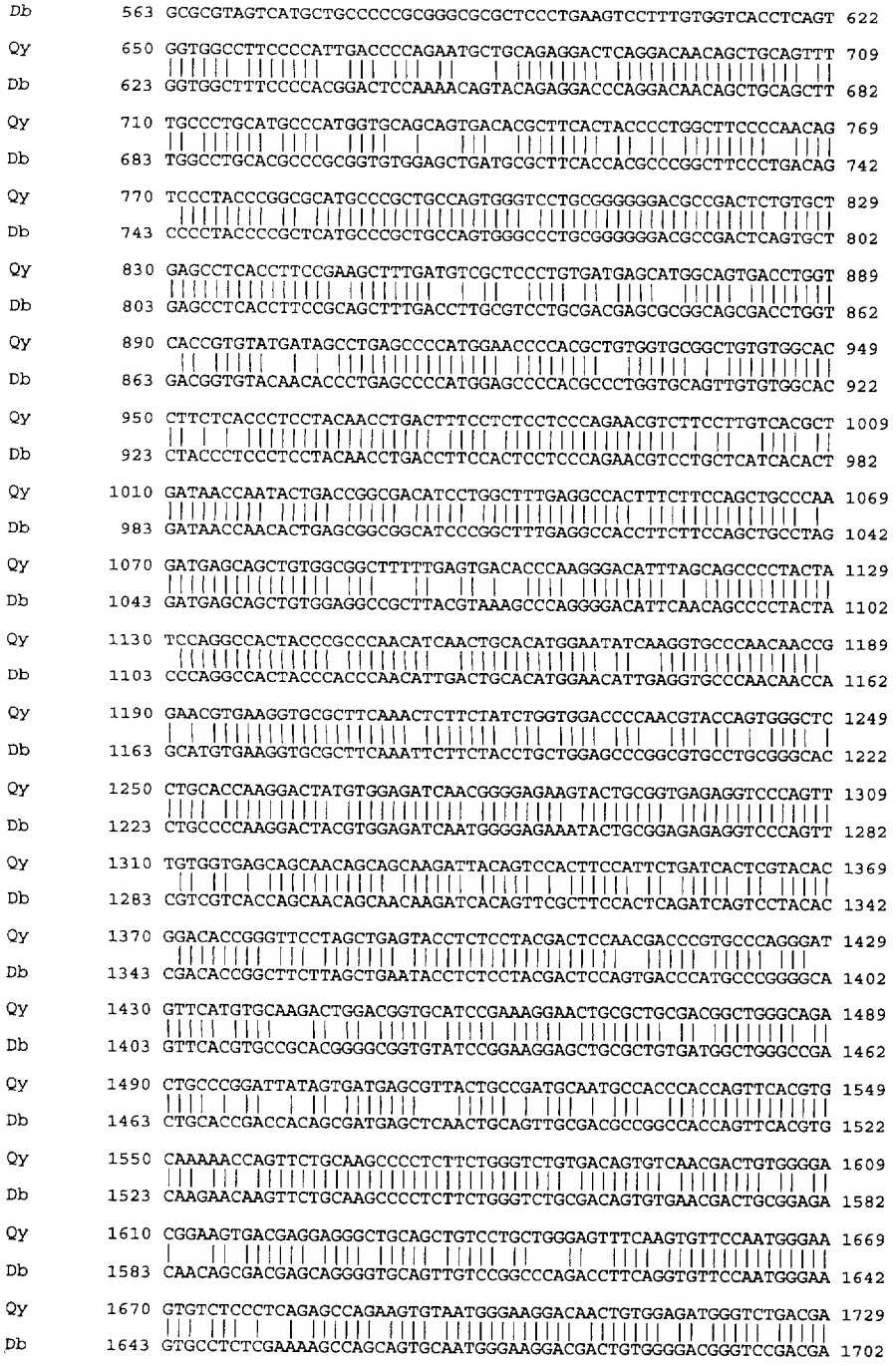
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Qy 770 TCCCTACCCGGCGCATGCCCGCTGCCAGTGGGTCCTGCGGGGGGACGCCGACTCTGTGCT 829
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Qy 890 CACCGTGTATGATAGCCTGAGCCCCATGGAACCCCACGCTGTGGTGCGGCTGTGTGGCAC 949
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Qy 950 CTTCTCACCCTCCTACAACCTGACTTTCCTCTCCTCCCAGAACGTCTTCCTTGTCACGCT 1009
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Qy 1010 GATAACCAATACTGACCGGCGACATCCTGGCTTTGAGGCCACTTTCTTCCAGCTGCCCAA 1069
Db 983 GATAACCAACACTGAGCGGCGGCATCCCGGCTTTGAGGCCACCTTCTTCCAGCTGCCTAG 1042
Qy 1070 GATGAGCAGCTGTGGCGGCTTTTTGAGTGACACCCAAGGGACATTTAGCAGCCCCTACTA 1129
Db 1043 GATGAGCAGCTGTGGAGGCCGCTTACGTAAAGCCCAGGGGACATTCAACAGCCCCTACTA 1102
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Qy 1190 GAACGTGAAGGTGCGCTTCAAACTCTTCTATCTGGTGGACCCCAACGTACCAGTGGGCTC 1249
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Db 2063 GGGCTTGCACGACCAGAGCCAGCGCAGCGCCCCTGGGGTGCAGGAGCGCAGGCTCAAGCG 2122
Qy 2150 TATCATCACCCACCCTTCCTTCAATGATTTCACCTTCGACTATGACATCGCCTTGCTGGA 2209
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Qy 2210 GCTGGAGAAGTCGGTGGAGTACAGCACCGTCGTGCGCCCCATCTGCCTGCCTGATGCTAC 2269
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Qy 2270 CCATGTCTTCCCTGCTGGCAAGGCCATCTGGGTCACAGGCTGGGGGCACACAAAAGAGGG 2329
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RESULT 3
US-09-776-191-1
; Sequence 1, Application US/09776191
; Publication No. US20030119168A1
; GENERAL INFORMATION:
; APPLICANT: Edwin L. Madison
; APPLICANT: Edgar O. Ong
; APPLICANT: Jiunn-Chern Yeh
; APPLICANT: Corvas International, Inc.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: TRANSMEMBRANE SERINE PROTEASES, THE ENCODED PROTEINS AND
; TITLE OF INVENTION: METHODS BASED THEREON
; FILE REFERENCE: 24745-1607
; CURRENT APPLICATION NUMBER: US/09/776,191
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/213,124
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/234,840
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/179,982
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 60/183,542
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: 09/657,968
; PRIOR FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 72
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; SEQ ID NO 1
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; ORGANISM: Homo Sapien
; FEATURE:
; OTHER INFORMATION: Nucleotide encoding MTSP1
; NAME/KEY: CDS
; LOCATION: (23)...(2589)
; PUBLICATION INFORMATION:
; AUTHORS: O'Brien, T.J. and Tanimoto, H.
; DATABASE ACCESSION NUMBER: GenBank AR081724
; PATENT DOCUMENT NUMBER: US Pat 5972616
; PATENT FILING DATE: 1998-02-20
; PUBLICATION DATE: 1999-10-26
US-09-776-191-1

Query Match 60.6%; Score 1883.2; DB 11; Length 3147;
Best Local Similarity 81.2%; Pred. No. 0;
Matches 2223; Conservative 0; Mismatches 508; Indels 5; Gaps 3;

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Db       185 TGGGTGGTGCTGGCAGCCGTGCTGATCGGCCTCCTCTTGGTCTTGCTGGGGATCGGCTTC 244

Qy       285 CTGGTGTGGCACTTCCATTATCGGAATGTGCGGGTTCAAAAAGTCTTCAATGGCCATCTG 344
             ||||||||||| ||  ||  ||  |||  |  |||||  ||  ||  ||  ||||||||||||  |   ||
Db       245 CTGGTGTGGCATTTGCAGTACCGGGACGTGCGTGTCCAGAAGGTCTTCAATGGCTACATG 304

Qy       345 AGGATCACAAATGAGATCTTTCTGGATGCGTATGAGAACTCCACCTCCACAGAGTTTATC 404
             ||||||||||||||   |||  |||||||  ||  ||||||||||  ||||||  ||||||  |
Db       305 AGGATCACAAATGAGAATTTTGTGGATGCCTACGAGAACTCCAACTCCACTGAGTTTGTA 364

Qy       405 AGCCTGGCCAGCCAGGTGAAGGAGGCGCTGAAGCTGCTGTACAATGAAGTCCCTGTCCTG 464
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Db       365 AGCCTGGCCAGCAAGGTGAAGGACGCGCTGAAGCTGCTGTACAGCGGAGTCCCATTCCTG 424

Qy       465 GGTCCCTACCACAAGAAGTCGGCTGTAACTGCCTTCAGTGAGGGCAGTGTCATCGCCTAC 524
             ||  ||||||||||| |||||||||  ||  |||||||  |||||||  ||||||||||||
Db       425 GGCCCCTACCACAAGGAGTCGGCTGTGACGGCCTTCAGCGAGGGCAGCGTCATCGCCTAC 484

Qy       525 TACTGGTCAGAGTTCAGCATCCCCCCACACCTGGCAGAAGAGGTTGATCGCGCCATGGCT 584
             |||||||  |||||||||||||  |  |||||||  ||  ||||  ||  ||||  ||||||
Db       485 TACTGGTCTGAGTTCAGCATCCCGCAGCACCTGGTGGAGGAGGCCGAGCGCGTCATGGCC 544

Qy       585 GTGGAGCGAGTTGTAACATTGCCACCCCGAGCACGGGCACTGAAATCCTTCGTGCTAACA 644
             |  ||||||  ||  ||  |   ||||  ||  ||  ||  ||  |  |||||  |||||  |||  |  ||
Db       545 GAGGAGCGCGTAGTCATGCTGCCCCCGCGGGCGCGCTCCCTGAAGTCCTTTGTGGTCACC 604

Qy       645 TCTGTGGTGGCCTTCCCCATTGACCCCAGAATGCTGCAGAGGACTCAGGACAACAGCTGC 704
             ||  ||||||||  |||||||   |||  |||  ||   |  ||||||||  ||||||||||||||||
Db       605 TCAGTGGTGGCTTTCCCCACGGACTCCAAAACAGTACAGAGGACCCAGGACAACAGCTGC 664

Qy       705 AGTTTTGCCCTGCATGCCCATGGTGCAGCAGTGACACGCTTCACTACCCCTGGCTTCCCC 764
             ||  ||||  ||||||  ||||   ||||  |  |||  ||||||||  ||  ||  ||||||||
Db       665 AGCTTTGGCCTGCACGCCCGCGGTGTGGAGCTGATGCGCTTCACCACGCCCGGCTTCCCT 724

Qy       765 AACAGTCCCTACCCGGCGCATGCCCGCTGCCAGTGGGTCCTGCGGGGGGGACGCCGACTCT 824
             ||||  ||||||||  ||  ||||||||||||||||||||  ||||||||||||||||||||
Db       725 GACAGCCCCTACCCCGCTCATGCCCGCTGCCAGTGGGCCCTGCGGGGGGGACGCCGACTCA 784

Qy       825 GTGCTGAGCCTCACCTTCCGAAGCTTTGATGTCGCTCCCTGTGATGAGCATGGCAGTGAC 884
             ||||||||||||||||||  |||||||  |  ||  ||||  ||  ||||  |||||  |||
Db       785 GTGCTGAGCCTCACCTTCCGCAGCTTTGACCTTGCGTCCTGCGACGAGCGCGGCAGCGAC 844

Qy       885 CTGGTCACCGTGTATGATAGCCTGAGCCCCATGGAACCCCACGCTGTGGTGCGGCTGTGT 944
             |||||  ||  |||||  |  |  ||||||||||||||||  |||||||  ||||||  |  |||||
Db       845 CTGGTGACGGTGTACAACACCCTGAGCCCCATGGAGCCCCACGCCCTGGTGCAGTTGTGT 904

Qy       945 GGCACCTTCTCACCCTCCTACAACCTGACTTTCCTCTCCTCCCAGAACGTCTTCCTTGTC 1004
             |||||||  |  ||||||||||||||||  ||||  ||||||||||||||||  |  ||  ||
Db       905 GGCACCTACCCTCCCTCCTACAACCTGACCTTCCACTCCTCCCAGAACGTCCTGCTCATC 964

Qy      1005 ACGCTGATAACCAATACTGACCGGCGACATCCTGGCTTTGAGGCCACTTTCTTCCAGCTG 1064
             ||  ||||||||||  |||||  |||||  |||||  ||||||||||||||||  ||||||||||
Db       965 ACACTGATAACCAACACTGAGCGGCGGCATCCCGGCTTTGAGGCCACCTTCTTCCAGCTG 1024

Qy      1065 CCCAAGATGAGCAGCTGTGGCGGCTTTTTGAGTGACACCCAAGGGACATTTAGCAGCCCC 1124
             ||  |  ||||||||||||||  |||   ||  ||  |  ||||  ||||||||  |  |||||||
Db      1025 CCTAGGATGAGCAGCTGTGGAGGCCGCTTACGTAAAGCCCAGGGGACATTCAACAGCCCC 1084

Qy      1125 TACTATCCAGGCCACTACCCGCCCAACATCAACTGCACATGGAATATCAAGGTGCCCAAC 1184
             |||||  ||||||||||||||  |||||||  ||||||||||||  ||  ||||||||||
Db      1085 TACTACCCAGGCCACTACCCACCCAACATTGACTGCACATGGAACATTGAGGTGCCCAAC 1144

Qy      1185 AACCGGAACGTGAAGGTGCGCTTCAAACTCTTCTATCTGGTGGACCCCAACGTACCAGTG 1244
             ||||  |  |||||||||  |||||||  |||  ||||  |||   |||  ||  ||  |  |
Db      1145 AACCAGCATGTGAAGGTGAGCTTCAAATTCTTCTACCTGCTGGAGCCCGGCGTGCCTGCG 1204

Qy      1245 GGCTCCTGCACCAAGGACTATGTGGAGATCAACGGGGAGAAGTACTGCGGTGAGAGGTCC 1304
             |||  |||||  ||||||||||  ||||||||||  |||||||  |||||||  |||||||||
Db      1205 GGCACCTGCCCCAAGGACTACGTGGAGATCAATGGGGAGAAATACTGCGGAGAGAGGTCC 1264

Qy      1305 CAGTTTGTGGTGAGCAGCAACAGCAGCAAGATTACAGTCCACTTCCATTCTGATCACTCG 1364
             ||||  ||  |  ||||||||||  ||||||  ||||  |  ||||||  ||  |||||  ||
Db      1265 CAGTTCGTCGTCACCAGCAACAGCAACAAGATCACAGTTCGCTTCCACTCAGATCAGTCC 1324

Qy      1365 TACACGGACACCGGGTTCCTAGCTGAGTACCTCTCCTACGACTCCAACGACCCGTGCCCA 1424
             ||||  ||||||||  |||  |||||||  ||||||||||||||||||  ||||||  ||||||
Db      1325 TACACCGACACCGGCTTCTTAGCTGAATACCTCTCCTACGACTCCAGTGACCCATGCCCG 1384

Qy      1425 GGGATGTTCATGTGCAAGACTGGACGGTGCATCCGAAAGGAACTGCGCTGCGACGGCTGG 1484
             |||  ||||  |||  ||  ||  |||||  ||||  |||||  ||||||||  ||  ||||||
Db      1385 GGGCAGTTCACGTGCCGCACGGGGCGGTGTATCCGGAAGGAGCTGCGCTGTGATGGCTGG 1444

Qy      1485 GCAGACTGCCCGGATTATAGTGATGAGCGTTACTGCCGATGCAATGCCACCCACCAGTTC 1544
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Db       1445 GCCGACTGCACCGACCACAGCGATGAGCTCAACTGCAGTTGCGACGCCGGCCACCAGTTC 1504

Qy       1545 ACGTGCAAAAACCAGTTCTGCAAGCCCCTCTTCTGGGTCTGTGACAGTGTCAACGACTGT 1604
Db       1505 ACGTGCAAGAACAAGTTCTGCAAGCCCCTCTTCTGGGTCTGCGACAGTGTGAACGACTGC 1564

Qy       1605 GGGGACGGAAGTGACGAGGAGGGCTGCAGCTGTCCTGCTGGGAGTTTCAAGTGTTCCAAT 1664
Db       1565 GGAGACAACAGCGACGAGCAGGGGTGCAGTTGTCCGGCCCAGACCTTCAGGTGTTCCAAT 1624

Qy       1665 GGGAAGTGTCTCCCTCAGAGCCAGAAGTGTAATGGGAAGGACAACTGTGGAGATGGGTCT 1724
Db       1625 GGGAAGTGCCTCTCGAAAAGCCAGCAGTGCAATGGGAAGGACGACTGTGGGGACGGGTCC 1684

Qy       1725 GACGAGGCTTCATGTGACAGCGTGAATGTCGTCTCTTGCACCAAATATACCTACCGCTGC 1784
Db       1685 GACGAGGCCTCCTGCCCCAAGGTGAACGTCGTCACTTGTACCAAACACACCTACCGCTGC 1744

Qy       1785 CAAAATGGCCTCTGTCTGAGCAAGGGCAACCCTGAGTGTGATGGGAAGACGGACTGTAGC 1844
Db       1745 CTCAATGGGCTCTGCTTGAGCAAGGGCAACCCTGAGTGTGACGGGAAGGAGGACTGTAGC 1804

Qy       1845 GATGGCTCCGATGAGAAAAACTGTGACTGTGGGCTGCGATCCTTTACCAAACAGGCTCGC 1904
Db       1805 GACGGCTCAGATGAGAAGGACTGCGACTGTGGGCTGCGGTCATTCACGAGACAGGCTCGT 1864

Qy       1905 GTGGTTGGTGGCACGAATGCGGACGAGGGCGAGTGGCCCTGGCAGGTGAGCCTCCACGCC 1964
Db       1865 GTTGTTGGGGGCACGGATGCGGATGAGGGCGAGTGGCCCTGGCAGGTAAGCCTGCATGCT 1924

Qy       1965 CTGGGCCAGGGCCACTTGTGTGGGGCCTCGCTCATCTCTCCTGACTGGCTGGTCTCTGCA 2024
Db       1925 CTGGGCCAGGGCCACATCTGCGGTGCTTCCCTCATCTCTCCCAACTGGCTGGTCTCTGCC 1984

Qy       2025 GCTCATTGCTTTCAGGATGACAAAAATTTCAAGTACTCAGACTACACGATGTGGACGGCC 2084
Db       1985 GCACACTGCTACATCGATGACAGAGGATTCAGGTACTCAGACCCCACGCAGTGGACGGCC 2044

Qy       2085 TTCCTGGGTCTGCTGGACCAGAGCAAGCGCAGTGCCTCTGGGGTGCAGGAGCTGAAGCTC 2144
Db       2045 TTCCTGGGCTTGCACGACCAGAGCCAGCGCAGCGCCCCTGGGGTGCAGGAGCGCAGGCTC 2104

Qy       2145 AAACGTATCATCACCCACCCTTCCTTCAATGATTTCACCTTCGACTATGACATCGCCTTG 2204
Db       2105 AAGCGCATCATCTCCCACCCCTTCTTCAATGACTTCACCTTCGACTATGACATCGCGCTG 2164

Qy       2205 CTGGAGCTGGAGAAGTCGGTGGAGTACAGCACCGTCGTGCGCCCCATCTGCCTGCCTGAT 2264
Db       2165 CTGGAGCTGGAGAAACCGGCAGAGTACAGCTCCATGGTGCGGCCCATCTGCCTGCCGGAC 2224

Qy       2265 GCTACCCATGTCTTCCCTGCTGGCAAGGCCATCTGGGTCACAGGCTGGGGGCACACAAAA 2324
Db       2225 GCCTCCCATGTCTTCCCTGCCGGCAAGGCCATCTGGGTCACGGGCTGGGGACACACCCAG 2284

Qy       2325 GAGGGAGGTACCGGAGCGCTGATCCTGCAGAAGGGTGAGATCCGTGTCATCAACCAGACC 2384
Db       2285 TATGGAGGCACTGGCGCGCTGATCCTGCAAAAGGGTGAGATCCGCGTCATCAACCAGACC 2344

Qy       2385 ACCTGTGAGGACCTCATGCCGCAGCAGATCACCCCACGAATGATGTGTGTGGGTTTCCTC 2444
Db       2345 ACCTGCGAGAACCTCCTGCCGCAGCAGATCACGCCGCGCATGATGTGCGTGGGCTTCCTC 2404

Qy       2445 AGTGGGGGTGTGGACTCCTGCCAGGGTGACTCTGGTGGCCCCTTGTCAAGCGCGGAGAAA 2504
Db       2405 AGCGGCGGCGTGGACTCCTGCCAGGGTGATTCCGGGGGACCCCTGTCCAGCGTGGAGGCG 2464

Qy       2505 GATGGGCGAATGTTCCAGGCTGGTGTGGTGAGCTGGGGTGAAGGCTGCGCTCAGAGGAAC 2564
Db       2465 GATGGGCGGATCTTCCAGGCCGGTGTGGTGAGCTGGGGAGACGGCTGCGCTCAGAGGAAC 2524

Qy       2565 AAGCCAGGCGTGTACACAAGGCTCCCTGTAGTTCGGGACTGGATCAAAGAGCACACTGGG 2624
Db       2525 AAGCCAGGCGTGTACACAAGGCTCCCTCTGTTTCGGGACTGGATCAAAGAGAACACTGGG 2584

Qy       2625 GTATAGCAGCATGGACAGACAGCCGACCACAAACACCCACAGGGATGCCCGACATGCACA 2684
Db       2585 GTATAGGGGCCGGG---GCCACCCAAATGTGTACACCTGCGGGGCCACCCATCGTCCACC 2641

Qy       2685 CCTGGATACAGGAGAGGAACACTGACGACATTTATGCTGTGGCCTCCCCCCCCCAACACA 2744
Db       2642 CCAGTGTGCACG-CCTGCAGGCTGGAGACTGGACCGCTGACTGCACCAGCGCCC-CCAGA 2699

Qy       2745 ACCCAGACTGTGAACTGCATCCTTAGGACTCAGAGT 2780
Db       2700 ACATACACTGTGAACTCAATCTCCAGGGCTCCAAAT 2735


RESULT 4
US-09-776-191-49
; Sequence 49, Application US/09776191
; Publication No. US20030119168A1
; GENERAL INFORMATION:
;  APPLICANT: Edwin L. Madison
;  APPLICANT:  Edgar O. Ong
;  APPLICANT:  Jiunn-Chern Yeh
;  APPLICANT:  Corvas International, Inc.
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
;  TITLE OF INVENTION:  TRANSMEMBRANE SERINE PROTEASES, THE ENCODED PROTEINS AND
;  TITLE OF INVENTION:  METHODS BASED THEREON
;  FILE REFERENCE: 24745-1607
;  CURRENT APPLICATION NUMBER: US/09/776,191
;  CURRENT FILING DATE:  2001-02-02
;  PRIOR APPLICATION NUMBER: 60/213,124
;  PRIOR FILING DATE: 2000-06-22
;  PRIOR APPLICATION NUMBER: 60/234,840
;  PRIOR FILING DATE: 2000-06-22
;  PRIOR APPLICATION NUMBER: 60/179,982
;  PRIOR FILING DATE: 2000-02-03
;  PRIOR APPLICATION NUMBER: 60/183,542
;  PRIOR FILING DATE: 2000-02-18
;  PRIOR APPLICATION NUMBER: 09/657,968
;  PRIOR FILING DATE: 2000-02-08
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 49
;   LENGTH: 3147
;   TYPE: DNA
;   ORGANISM: Homo Sapien
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1865)...(2590)
;   OTHER INFORMATION: Nucleic acid sequence of protease domain of MTSP1
US-09-776-191-49

  Query Match            60.6%;  Score 1883.2;  DB 11;  Length 3147;
  Best Local Similarity  81.2%;  Pred. No. 0;
  Matches 2223;  Conservative    0;  Mismatches  508;  Indels    5;  Gaps    3;

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Db          5 GAGCGGCCTCGGGGTACCATGGGGAGCGATCGGGCCCGCAAGGGCGGAGGGGGCCCGAAG 64

Qy        105 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCTAGAGAACATGAATGGCTTTGAGGAG 164
Db         65 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCACGAGAAAGTGAATGGCTTGGAGGAA 124

Qy        165 GGTGTGGAGTTCCTGCCTGCGAACAATGCCAAGAAAGTGGAGAAGCGAGGCCCCAGGCGC 224
Db        125 GGCGTGGAGTTCCTGCCAGTCAACAACGTCAAGAAGGTGGAAAAGCATGGCCCGGGGCGC 184

Qy        225 TGGGTGGTGCTGGTGGCAGTGCTGTTCAGCTTCCTCTTGCTCTCCCTCATGGCTGGCTTG 284
Db        185 TGGGTGGTGCTGGCAGCCGTGCTGATCGGCCTCCTCTTGGTCTTGCTGGGGATCGGCTTC 244

Qy        285 CTGGTGTGGCACTTCCATTATCGGAATGTGCGGGTTCAAAAAGTCTTCAATGGCCATCTG 344
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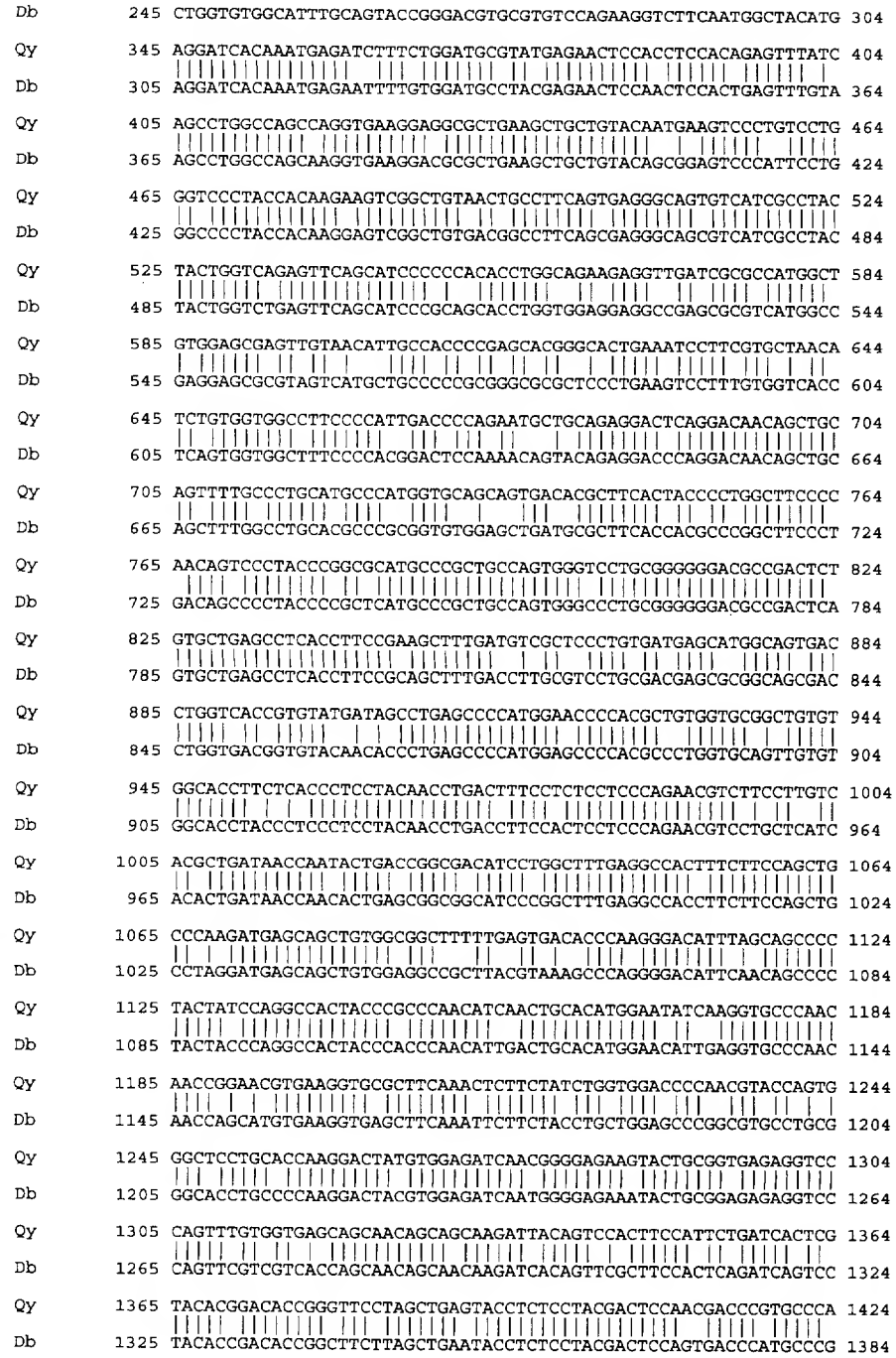
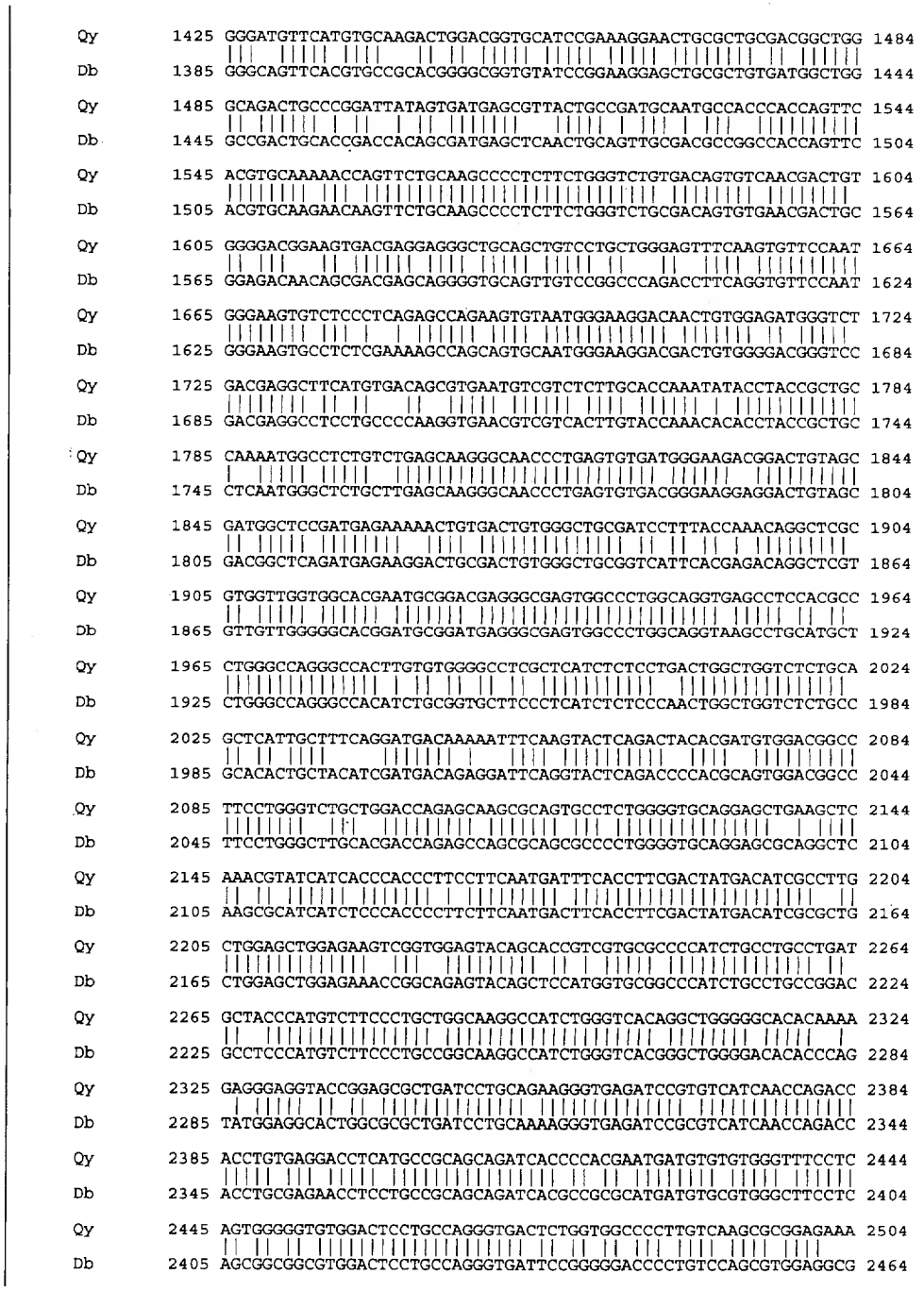
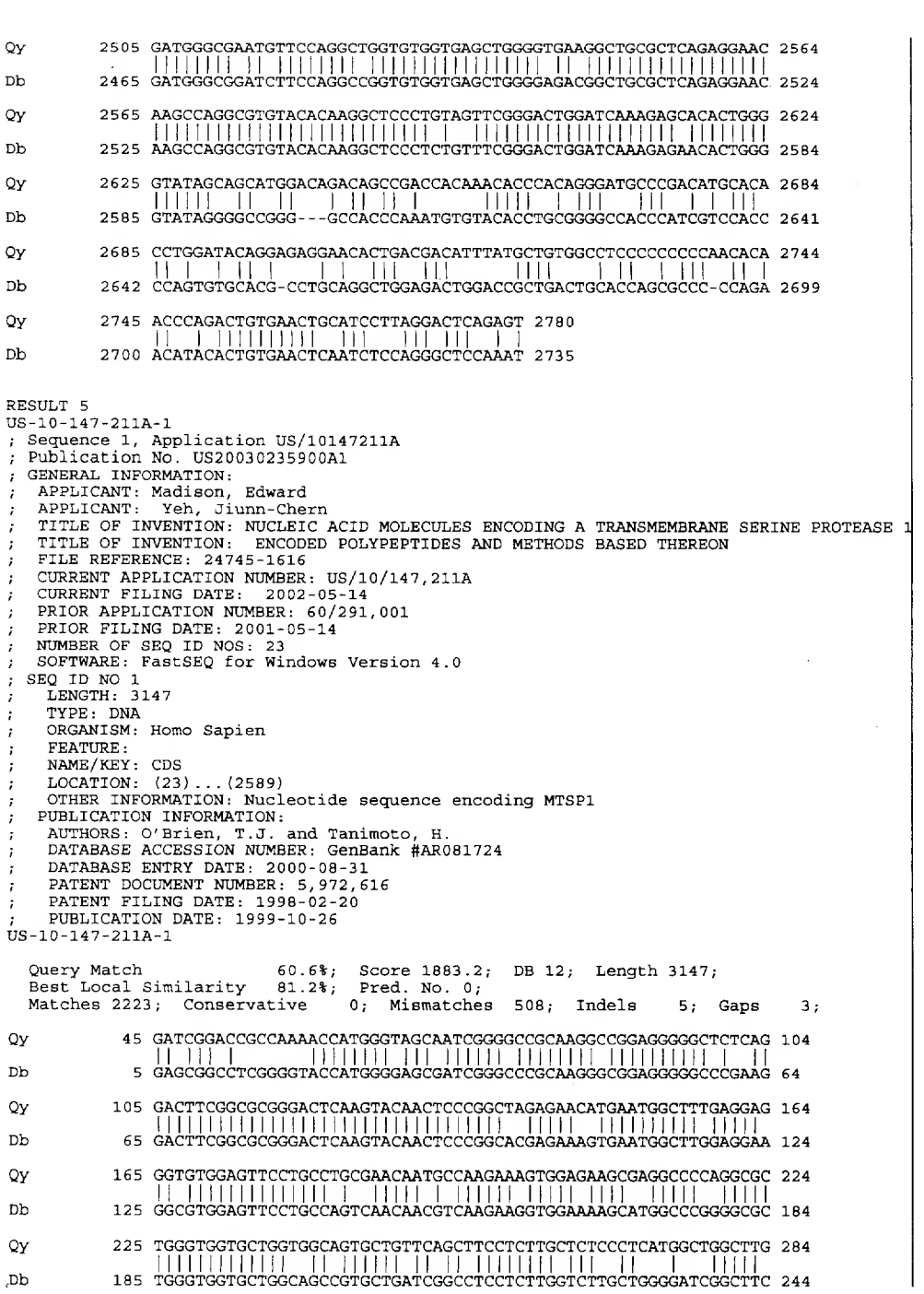
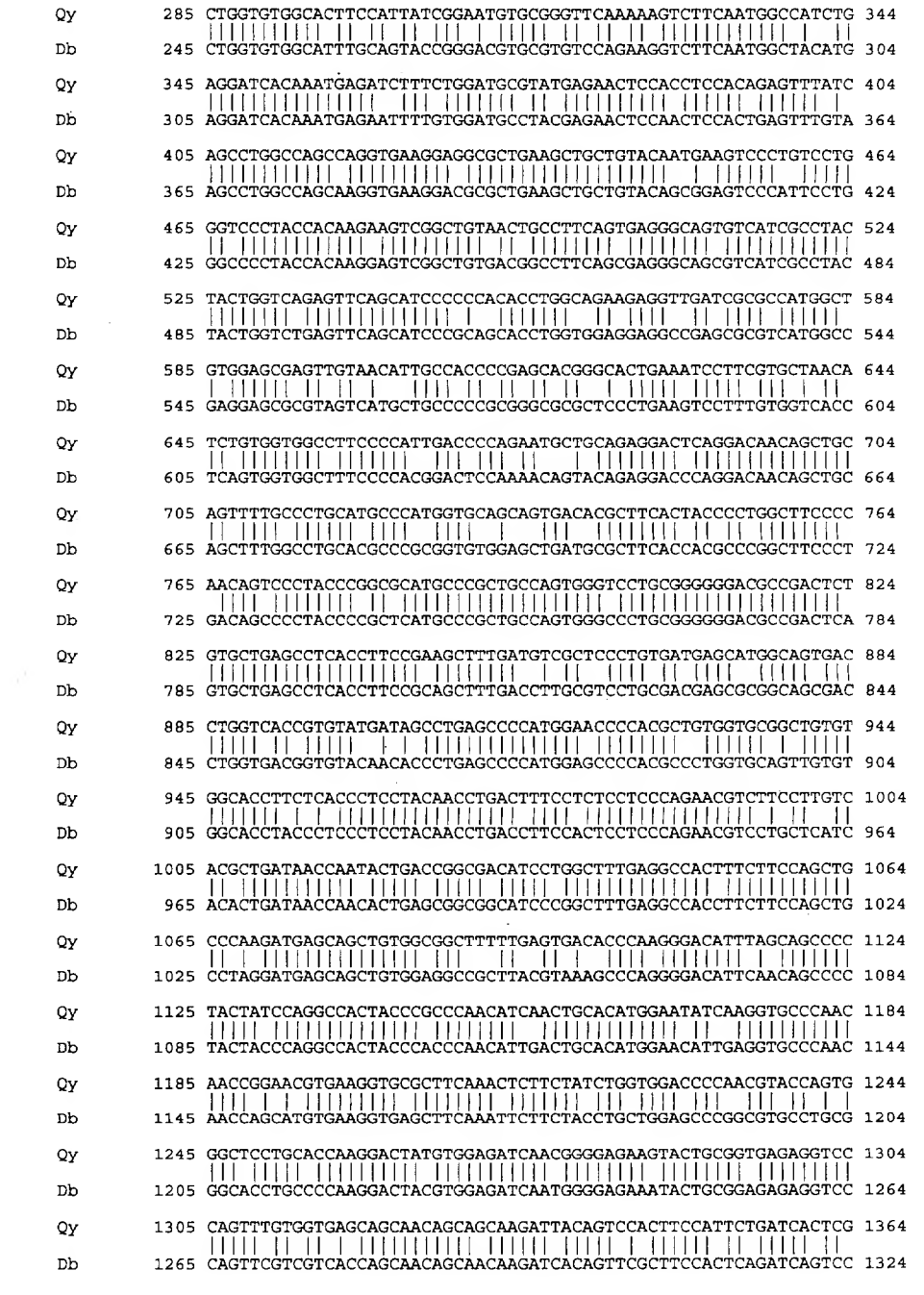






RESULT 5
US-10-147-211A-1
; Sequence 1, Application US/10147211A
; Publication No. US20030235900A1
; GENERAL INFORMATION:
; APPLICANT: Madison, Edward
; APPLICANT: Yeh, Jiunn-Chern
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING A TRANSMEMBRANE SERINE PROTEASE 1
; TITLE OF INVENTION: ENCODED POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: 24745-1616
; CURRENT APPLICATION NUMBER: US/10/147,211A
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/291,001
; PRIOR FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3147
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (23)...(2589)
; OTHER INFORMATION: Nucleotide sequence encoding MTSP1
; PUBLICATION INFORMATION:
; AUTHORS: O'Brien, T.J. and Tanimoto, H.
; DATABASE ACCESSION NUMBER: GenBank #AR081724
; DATABASE ENTRY DATE: 2000-08-31
; PATENT DOCUMENT NUMBER: 5,972,616
; PATENT FILING DATE: 1998-02-20
; PUBLICATION DATE: 1999-10-26
US-10-147-211A-1

Query Match 60.6%; Score 1883.2; DB 12; Length 3147;
Best Local Similarity 81.2%; Pred. No. 0;
Matches 2223; Conservative 0; Mismatches 508; Indels 5; Gaps 3;



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Db       1325 TACACCGACACCGGCTTCTTAGCTGAATACCTCTCCTACGACTCCAGTGACCCATGCCCG 1384

Qy       1425 GGGATGTTCATGTGCAAGACTGGACGGTGCATCCGAAAGGAACTGCGCTGCGACGGCTGG 1484
Db       1385 GGGCAGTTCACGTGCCGCACGGGGCGGTGTATCCGGAAGGAGCTGCGCTGTGATGGCTGG 1444

Qy       1485 GCAGACTGCCCGGATTATAGTGATGAGCGTTACTGCCGATGCAATGCCACCCACCAGTTC 1544
Db       1445 GCCGACTGCACCGACCACAGCGATGAGCTCAACTGCAGTTGCGACGCCGGCCACCAGTTC 1504

Qy       1545 ACGTGCAAAAACCAGTTCTGCAAGCCCCTCTTCTGGGTCTGTGACAGTGTCAACGACTGT 1604
Db       1505 ACGTGCAAGAACAAGTTCTGCAAGCCCCTCTTCTGGGTCTGCGACAGTGTGAACGACTGC 1564

Qy       1605 GGGGACGGAAGTGACGAGGAGGGCTGCAGCTGTCCTGCTGGGAGTTTCAAGTGTTCCAAT 1664
Db       1565 GGAGACAACAGCGACGAGCAGGGGTGCAGTTGTCCGGCCCAGACCTTCAGGTGTTCCAAT 1624

Qy       1665 GGGAAGTGTCTCCCTCAGAGCCAGAAGTGTAATGGGAAGGACAACTGTGGAGATGGGTCT 1724
Db       1625 GGGAAGTGCCTCTCGAAAAGCCAGCAGTGCAATGGGAAGGACGACTGTGGGGACGGGTCC 1684

Qy       1725 GACGAGGCTTCATGTGACAGCGTGAATGTCGTCTCTTGCACCAAATATACCTACCGCTGC 1784
Db       1685 GACGAGGCCTCCTGCCCCAAGGTGAACGTCGTCACTTGTACCAAACACACCTACCGCTGC 1744

Qy       1785 CAAAATGGCCTCTGTCTGAGCAAGGGCAACCCTGAGTGTGATGGGAAGACGGACTGTAGC 1844
Db       1745 CTCAATGGGCTCTGCTTGAGCAAGGGCAACCCTGAGTGTGACGGGAAGGAGGACTGTAGC 1804

Qy       1845 GATGGCTCCGATGAGAAAAACTGTGACTGTGGGCTGCGATCCTTTACCAAACAGGCTCGC 1904
Db       1805 GACGGCTCAGATGAGAAGGACTGCGACTGTGGGCTGCGGTCATTCACGAGACAGGCTCGT 1864

Qy       1905 GTGGTTGGTGGCACGAATGCGGACGAGGGCGAGTGGCCCTGGCAGGTGAGCCTCCACGCC 1964
Db       1865 GTTGTTGGGGGCACGGATGCGGATGAGGGCGAGTGGCCCTGGCAGGTAAGCCTGCATGCT 1924

Qy       1965 CTGGGCCAGGGCCACTTGTGTGGGGCCTCGCTCATCTCTCCTGACTGGCTGGTCTCTGCA 2024
Db       1925 CTGGGCCAGGGCCACATCTGCGGTGCTTCCCTCATCTCTCCCAACTGGCTGGTCTCTGCC 1984

Qy       2025 GCTCATTGCTTTCAGGATGACAAAAATTTCAAGTACTCAGACTACACGATGTGGACGGCC 2084
Db       1985 GCACACTGCTACATCGATGACAGAGGATTCAGGTACTCAGACCCCACGCAGTGGACGGCC 2044

Qy       2085 TTCCTGGGTCTGCTGGACCAGAGCAAGCGCAGTGCCTCTGGGGTGCAGGAGCTGAAGCTC 2144
Db       2045 TTCCTGGGCTTGCACGACCAGAGCCAGCGCAGCGCCCCTGGGGTGCAGGAGCGCAGGCTC 2104

Qy       2145 AAACGTATCATCACCCACCCTTCCTTCAATGATTTCACCTTCGACTATGACATCGCCTTG 2204
Db       2105 AAGCGCATCATCTCCCACCCCTTCTTCAATGACTTCACCTTCGACTATGACATCGCGCTG 2164

Qy       2205 CTGGAGCTGGAGAAGTCGGTGGAGTACAGCACCGTCGTGCGCCCCATCTGCCTGCCTGAT 2264
Db       2165 CTGGAGCTGGAGAAACCGGCAGAGTACAGCTCCATGGTGCGGCCCATCTGCCTGCCGGAC 2224

Qy       2265 GCTACCCATGTCTTCCCTGCTGGCAAGGCCATCTGGGTCACAGGCTGGGGGCACACAAAA 2324
Db       2225 GCCTCCCATGTCTTCCCTGCCGGCAAGGCCATCTGGGTCACGGGCTGGGGACACACCCAG 2284

Qy       2325 GAGGGAGGTACCGGAGCGCTGATCCTGCAGAAGGGTGAGATCCGTGTCATCAACCAGACC 2384
Db       2285 TATGGAGGCACTGGCGCGCTGATCCTGCAAAAGGGTGAGATCCGCGTCATCAACCAGACC 2344

Qy       2385 ACCTGTGAGGACCTCATGCCGCAGCAGATCACCCCACGAATGATGTGTGTGGGTTTCCTC 2444
Db       2345 ACCTGCGAGAACCTCCTGCCGCAGCAGATCACGCCGCGCATGATGTGCGTGGGCTTCCTC 2404

Qy       2445 AGTGGGGGTGTGGACTCCTGCCAGGGTGACTCTGGTGGCCCCTTGTCAAGCGCGGAGAAA 2504

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Db       2405 AGCGGCGGCGTGGACTCCTGCCAGGGTGATTCCGGGGGACCCCTGTCCAGCGTGGAGGCG 2464

Qy       2505 GATGGGCGAATGTTCCAGGCTGGTGTGGTGAGCTGGGGTGAAGGCTGCGCTCAGAGGAAC 2564
Db       2465 GATGGGCGGATCTTCCAGGCCGGTGTGGTGAGCTGGGGAGACGGCTGCGCTCAGAGGAAC 2524

Qy       2565 AAGCCAGGCGTGTACACAAGGCTCCCTGTAGTTCGGGACTGGATCAAAGAGCACACTGGG 2624
Db       2525 AAGCCAGGCGTGTACACAAGGCTCCCTCTGTTTCGGGACTGGATCAAAGAGAACACTGGG 2584

Qy       2625 GTATAGCAGCATGGACAGACAGCCGACCACAAACACCCACAGGGATGCCCGACATGCACA 2684
Db       2585 GTATAGGGGCCGGG---GCCACCCAAATGTGTACACCTGCGGGGCCACCCATCGTCCACC 2641

Qy       2685 CCTGGATACAGGAGAGGAACACTGACGACATTTATGCTGTGGCCTCCCCCCCCCAACACA 2744
Db       2642 CCAGTGTGCACG-CCTGCAGGCTGGAGACTGGACCGCTGACTGCACCAGCGCCC-CCAGA 2699

Qy       2745 ACCCAGACTGTGAACTGCATCCTTAGGACTCAGAGT 2780
Db       2700 ACATACACTGTGAACTCAATCTCCAGGGCTCCAAAT 2735
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RESULT 6
US-10-147-211A-3
; Sequence 3, Application US/10147211A
; Publication No. US20030235900A1
; GENERAL INFORMATION:
; APPLICANT: Madison, Edward
; APPLICANT: Yeh, Jiunn-Chern
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING A TRANSMEMBRANE SERINE PROTEASE 1(
; TITLE OF INVENTION: ENCODED POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: 24745-1616
; CURRENT APPLICATION NUMBER: US/10/147,211A
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/291,001
; PRIOR FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3147
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1865)...(2590)
; OTHER INFORMATION: Nucleic acid sequence of protease domain of MTSP1
US-10-147-211A-3

Query Match 60.6%; Score 1883.2; DB 12; Length 3147;
Best Local Similarity 81.2%; Pred. No. 0;
Matches 2223; Conservative 0; Mismatches 508; Indels 5; Gaps 3;

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Db          5 GAGCGGCCTCGGGGTACCATGGGGAGCGATCGGGCCCGCAAGGGCGGAGGGGGCCCGAAG 64

Qy        105 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCTAGAGAACATGAATGGCTTTGAGGAG 164
Db         65 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCACGAGAAAGTGAATGGCTTGGAGGAA 124

Qy        165 GGTGTGGAGTTCCTGCCTGCGAACAATGCCAAGAAAGTGGAGAAGCGAGGCCCCAGGCGC 224
Db        125 GGCGTGGAGTTCCTGCCAGTCAACAACGTCAAGAAGGTGGAAAAGCATGGCCCGGGGCGC 184

Qy        225 TGGGTGGTGCTGGTGGCAGTGCTGTTCAGCTTCCTCTTGCTCTCCCTCATGGCTGGCTTG 284
Db        185 TGGGTGGTGCTGGCAGCCGTGCTGATCGGCCTCCTCTTGGTCTTGCTGGGGATCGGCTTC 244

Qy        285 CTGGTGTGGCACTTCCATTATCGGAATGTGCGGGTTCAAAAAGTCTTCAATGGCCATCTG 344
Db        245 CTGGTGTGGCATTTGCAGTACCGGGACGTGCGTGTCCAGAAGGTCTTCAATGGCTACATG 304
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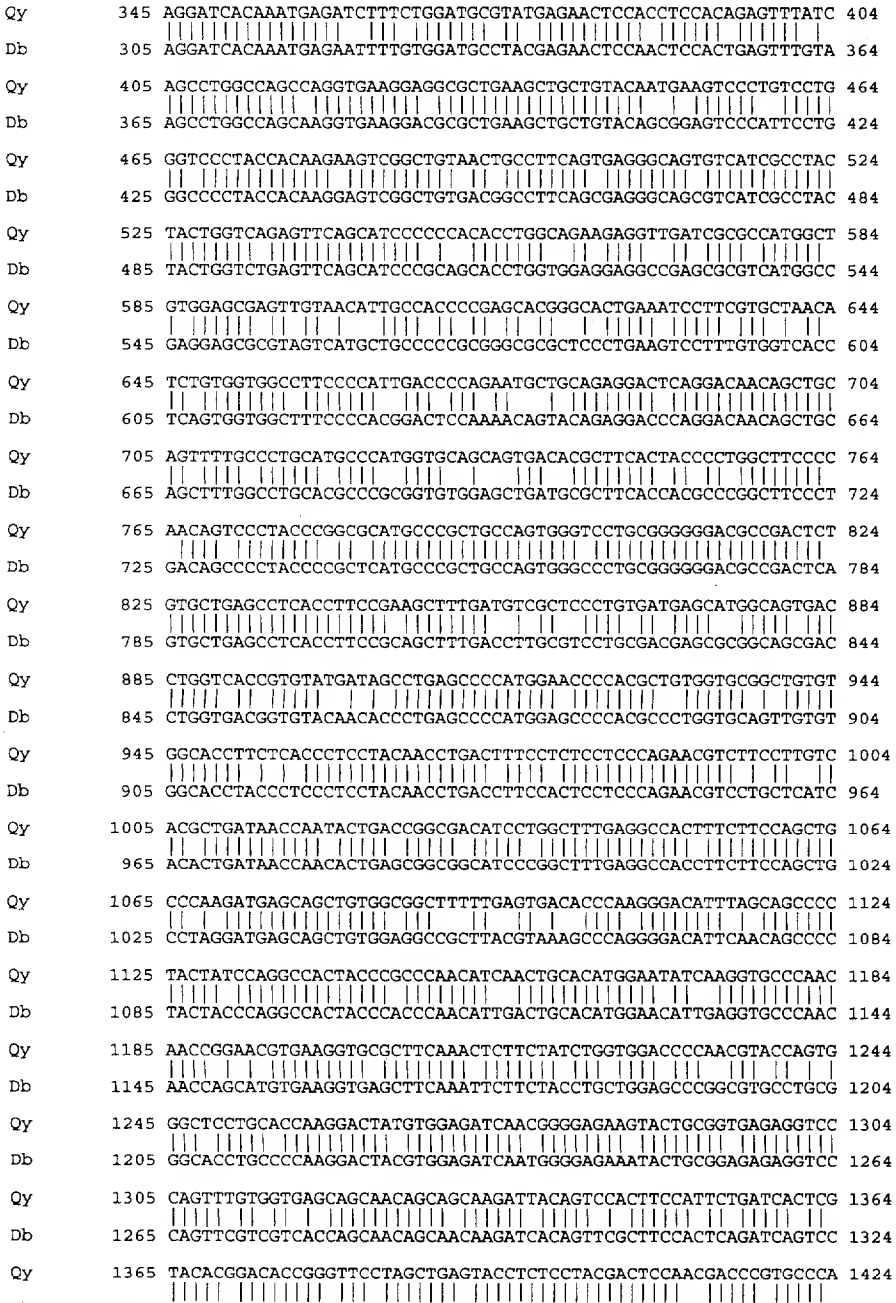
Qy 345 AGGATCACAAATGAGATCTTTCTGGATGCGTATGAGAACTCCACCTCCACAGAGTTTATC 404
Db 305 AGGATCACAAATGAGAATTTTGTGGATGCCTACGAGAACTCCAACTCCACTGAGTTTGTA 364
Qy 405 AGCCTGGCCAGCCAGGTGAAGGAGGCGCTGAAGCTGCTGTACAATGAAGTCCCTGTCCTG 464
Db 365 AGCCTGGCCAGCAAGGTGAAGGACGCGCTGAAGCTGCTGTACAGCGGAGTCCCATTCCTG 424
Qy 465 GGTCCCTACCACAAGAAGTCGGCTGTAACTGCCTTCAGTGAGGGCAGTGTCATCGCCTAC 524
Db 425 GGCCCCTACCACAAGGAGTCGGCTGTGACGGCCTTCAGCGAGGGCAGCGTCATCGCCTAC 484
Qy 525 TACTGGTCAGAGTTCAGCATCCCCCCACACCTGGCAGAAGAGGTTGATCGCGCCATGGCT 584
Db 485 TACTGGTCTGAGTTCAGCATCCCGCAGCACCTGGTGGAGGAGGCCGAGCGCGTCATGGCC 544
Qy 585 GTGGAGCGAGTTGTAACATTGCCACCCCGAGCACGGGCACTGAAATCCTTCGTGCTAACA 644
Db 545 GAGGAGCGCGTAGTCATGCTGCCCCCGCGGGCGCGCTCCCTGAAGTCCTTTGTGGTCACC 604
Qy 645 TCTGTGGTGGCCTTCCCCATTGACCCCAGAATGCTGCAGAGGACTCAGGACAACAGCTGC 704
Db 605 TCAGTGGTGGCTTTCCCCACGGACTCCAAAACAGTACAGAGGACCCAGGACAACAGCTGC 664
Qy 705 AGTTTTGCCCTGCATGCCCATGGTGCAGCAGTGACACGCTTCACTACCCCTGGCTTCCCC 764
Db 665 AGCTTTGGCCTGCACGCCCGCGGTGTGGAGCTGATGCGCTTCACCACGCCCGGCTTCCCT 724
Qy 765 AACAGTCCCTACCCGGCGCATGCCCGCTGCCAGTGGGTCCTGCGGGGGGACGCCGACTCT 824
Db 725 GACAGCCCCTACCCCGCTCATGCCCGCTGCCAGTGGGCCCTGCGGGGGGACGCCGACTCA 784
Qy 825 GTGCTGAGCCTCACCTTCCGAAGCTTTGATGTCGCTCCCTGTGATGAGCATGGCAGTGAC 884
Db 785 GTGCTGAGCCTCACCTTCCGCAGCTTTGACCTTGCGTCCTGCGACGAGCGCGGCAGCGAC 844
Qy 885 CTGGTCACCGTGTATGATAGCCTGAGCCCCATGGAACCCCACGCTGTGGTGCGGCTGTGT 944
Db 845 CTGGTGACGGTGTACAACACCCTGAGCCCCATGGAGCCCCACGCCCTGGTGCAGTTGTGT 904
Qy 945 GGCACCTTCTCACCCTCCTACAACCTGACTTTCCTCTCCTCCCAGAACGTCTTCCTTGTC 1004
Db 905 GGCACCTACCCTCCCTCCTACAACCTGACCTTCCACTCCTCCCAGAACGTCCTGCTCATC 964
Qy 1005 ACGCTGATAACCAATACTGACCGGCGACATCCTGGCTTTGAGGCCACTTTCTTCCAGCTG 1064
Db 965 ACACTGATAACCAACACTGAGCGGCGGCATCCCGGCTTTGAGGCCACCTTCTTCCAGCTG 1024
Qy 1065 CCCAAGATGAGCAGCTGTGGCGGCTTTTTGAGTGACACCCAAGGGACATTTAGCAGCCCC 1124
Db 1025 CCTAGGATGAGCAGCTGTGGAGGCCGCTTACGTAAAGCCCAGGGGACATTCAACAGCCCC 1084
Qy 1125 TACTATCCAGGCCACTACCCGCCCAACATCAACTGCACATGGAATATCAAGGTGCCCAAC 1184
Db 1085 TACTACCCAGGCCACTACCCACCCAACATTGACTGCACATGGAACATTGAGGTGCCCAAC 1144
Qy 1185 AACCGGAACGTGAAGGTGCGCTTCAAACTCTTCTATCTGGTGGACCCCAACGTACCAGTG 1244
Db 1145 AACCAGCATGTGAAGGTGAGCTTCAAATTCTTCTACCTGCTGGAGCCCGGCGTGCCTGCG 1204
Qy 1245 GGCTCCTGCACCAAGGACTATGTGGAGATCAACGGGGAGAAGTACTGCGGTGAGAGGTCC 1304
Db 1205 GGCACCTGCCCCAAGGACTACGTGGAGATCAATGGGGAGAAATACTGCGGAGAGAGGTCC 1264
Qy 1305 CAGTTTGTGGTGAGCAGCAACAGCAGCAAGATTACAGTCCACTTCCATTCTGATCACTCG 1364
Db 1265 CAGTTCGTCGTCACCAGCAACAGCAACAAGATCACAGTTCGCTTCCACTCAGATCAGTCC 1324
Qy 1365 TACACGGACACCGGGTTCCTAGCTGAGTACCTCTCCTACGACTCCAACGACCCGTGCCCA 1424
Db 1325 TACACCGACACCGGCTTCTTAGCTGAATACCTCTCCTACGACTCCAGTGACCCATGCCCG 1384
Qy 1425 GGGATGTTCATGTGCAAGACTGGACGGTGCATCCGAAAGGAACTGCGCTGCGACGGCTGG 1484
Db 1385 GGGCAGTTCACGTGCCGCACGGGGCGGTGTATCCGGAAGGAGCTGCGCTGTGATGGCTGG 1444
Qy 1485 GCAGACTGCCCGGATTATAGTGATGAGCGTTACTGCCGATGCAATGCCACCCACCAGTTC 1544
Db 1445 GCCGACTGCACCGACCACAGCGATGAGCTCAACTGCAGTTGCGACGCCGGCCACCAGTTC 1504
Qy 1545 ACGTGCAAAAACCAGTTCTGCAAGCCCCTCTTCTGGGTCTGTGACAGTGTCAACGACTGT 1604
Db 1505 ACGTGCAAGAACAAGTTCTGCAAGCCCCTCTTCTGGGTCTGCGACAGTGTGAACGACTGC 1564
Qy 1605 GGGGACGGAAGTGACGAGGAGGGCTGCAGCTGTCCTGCTGGGAGTTTCAAGTGTTCCAAT 1664
Db 1565 GGAGACAACAGCGACGAGCAGGGGTGCAGTTGTCCGGCCCAGACCTTCAGGTGTTCCAAT 1624
Qy 1665 GGGAAGTGTCTCCCTCAGAGCCAGAAGTGTAATGGGAAGGACAACTGTGGAGATGGGTCT 1724
Db 1625 GGGAAGTGCCTCTCGAAAAGCCAGCAGTGCAATGGGAAGGACGACTGTGGGGACGGGTCC 1684
Qy 1725 GACGAGGCTTCATGTGACAGCGTGAATGTCGTCTCTTGCACCAAATATACCTACCGCTGC 1784
Db 1685 GACGAGGCCTCCTGCCCCAAGGTGAACGTCGTCACTTGTACCAAACACACCTACCGCTGC 1744
Qy 1785 CAAAATGGCCTCTGTCTGAGCAAGGGCAACCCTGAGTGTGATGGGAAGACGGACTGTAGC 1844
Db 1745 CTCAATGGGCTCTGCTTGAGCAAGGGCAACCCTGAGTGTGACGGGAAGGAGGACTGTAGC 1804
Qy 1845 GATGGCTCCGATGAGAAAAACTGTGACTGTGGGCTGCGATCCTTTACCAAACAGGCTCGC 1904
Db 1805 GACGGCTCAGATGAGAAGGACTGCGACTGTGGGCTGCGGTCATTCACGAGACAGGCTCGT 1864
Qy 1905 GTGGTTGGTGGCACGAATGCGGACGAGGGCGAGTGGCCCTGGCAGGTGAGCCTCCACGCC 1964
Db 1865 GTTGTTGGGGGCACGGATGCGGATGAGGGCGAGTGGCCCTGGCAGGTAAGCCTGCATGCT 1924
Qy 1965 CTGGGCCAGGGCCACTTGTGTGGGGCCTCGCTCATCTCTCCTGACTGGCTGGTCTCTGCA 2024
Db 1925 CTGGGCCAGGGCCACATCTGCGGTGCTTCCCTCATCTCTCCCAACTGGCTGGTCTCTGCC 1984
Qy 2025 GCTCATTGCTTTCAGGATGACAAAAATTTCAAGTACTCAGACTACACGATGTGGACGGCC 2084
Db 1985 GCACACTGCTACATCGATGACAGAGGATTCAGGTACTCAGACCCCACGCAGTGGACGGCC 2044
Qy 2085 TTCCTGGGTCTGCTGGACCAGAGCAAGCGCAGTGCCTCTGGGGTGCAGGAGCTGAAGCTC 2144
Db 2045 TTCCTGGGCTTGCACGACCAGAGCCAGCGCAGCGCCCCTGGGGTGCAGGAGCGCAGGCTC 2104
Qy 2145 AAACGTATCATCACCCACCCTTCCTTCAATGATTTCACCTTCGACTATGACATCGCCTTG 2204
Db 2105 AAGCGCATCATCTCCCACCCCTTCTTCAATGACTTCACCTTCGACTATGACATCGCGCTG 2164
Qy 2205 CTGGAGCTGGAGAAGTCGGTGGAGTACAGCACCGTCGTGCGCCCCATCTGCCTGCCTGAT 2264
Db 2165 CTGGAGCTGGAGAAACCGGCAGAGTACAGCTCCATGGTGCGGCCCATCTGCCTGCCGGAC 2224
Qy 2265 GCTACCCATGTCTTCCCTGCTGGCAAGGCCATCTGGGTCACAGGCTGGGGGCACACAAAA 2324
Db 2225 GCCTCCCATGTCTTCCCTGCCGGCAAGGCCATCTGGGTCACGGGCTGGGGACACACCCAG 2284
Qy 2325 GAGGGAGGTACCGGAGCGCTGATCCTGCAGAAGGGTGAGATCCGTGTCATCAACCAGACC 2384
Db 2285 TATGGAGGCACTGGCGCGCTGATCCTGCAAAAGGGTGAGATCCGCGTCATCAACCAGACC 2344
Qy 2385 ACCTGTGAGGACCTCATGCCGCAGCAGATCACCCCACGAATGATGTGTGTGGGTTTCCTC 2444
Db 2345 ACCTGCGAGAACCTCCTGCCGCAGCAGATCACGCCGCGCATGATGTGCGTGGGCTTCCTC 2404
Qy 2445 AGTGGGGGTGTGGACTCCTGCCAGGGTGACTCTGGTGGCCCCTTGTCAAGCGCGGAGAAA 2504
Db 2405 AGCGGCGGCGTGGACTCCTGCCAGGGTGATTCCGGGGGACCCCTGTCCAGCGTGGAGGCG 2464
Qy 2505 GATGGGCGAATGTTCCAGGCTGGTGTGGTGAGCTGGGGTGAAGGCTGCGCTCAGAGGAAC 2564

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Db       2465 GATGGGCGGATCTTCCAGGCCGGTGTGGTGAGCTGGGGAGACGGCTGCGCTCAGAGGAAC 2524

Qy       2565 AAGCCAGGCGTGTACACAAGGCTCCCTGTAGTTCGGGACTGGATCAAAGAGCACACTGGG 2624

Db       2525 AAGCCAGGCGTGTACACAAGGCTCCCTCTGTTTCGGGACTGGATCAAAGAGAACACTGGG 2584

Qy       2625 GTATAGCAGCATGGACAGACAGCCGACCACAAACACCCACAGGGATGCCCGACATGCACA 2684

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Db       2642 CCAGTGTGCACG-CCTGCAGGCTGGAGACCGCTGACTGCACCAGCGCCC-CCAGA 2699

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Db       2700 ACATACACTGTGAACTCAATCTCCAGGGCTCCAAAT 2735
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RESULT 7
US-10-156-214A-1
; Sequence 1, Application US/10156214A
; Publication No. US20040001801A1
; GENERAL INFORMATION:
; APPLICANT: Edwin L. Madison
; APPLICANT: Joseph Edward Semple
; APPLICANT: George P. Vlasuk
; APPLICANT: Scott Jeffrey Kemp
; APPLICANT: Mallareddy Komandla
; APPLICANT: Daniel Vanna Siev
; TITLE OF INVENTION: Conjugates Activated By Cell Surface Proteases and Therapeutic Us
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 24745-1611
; CURRENT APPLICATION NUMBER: US/10/156,214A
; CURRENT FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 611
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3147
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (23)...(2589)
; OTHER INFORMATION: Nucleotide sequence encoding MTSP1
; PUBLICATION INFORMATION:
; AUTHORS: O'Brien, T.J. and Tanimoto, H.
; DATABASE ACCESSION NUMBER: GenBank AR081724
; DATABASE ENTRY DATE: 2000-08-31
; PATENT DOCUMENT NUMBER: US Pat 5972616
; PATENT FILING DATE: 1998-02-20
; PUBLICATION DATE: 1999-10-26
US-10-156-214A-1

Query Match 60.6%; Score 1883.2; DB 12; Length 3147;
Best Local Similarity 81.2%; Pred. No. 0;
Matches 2223; Conservative 0; Mismatches 508; Indels 5; Gaps 3;

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Qy         45 GATCGGACCGCCAAAACCATGGGTAGCAATCGGGGCCGCAAGGCCGGAGGGGGCTCTCAG 104

Db          5 GAGCGGCCTCGGGGTACCATGGGGAGCGATCGGGCCCGCAAGGGCGGAGGGGGCCCGAAG 64

Qy        105 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCTAGAGAACATGAATGGCTTTGAGGAG 164

Db         65 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCACGAGAAAGTGAATGGCTTGGAGGAA 124

Qy        165 GGTGTGGAGTTCCTGCCTGCGAACAATGCCAAGAAAGTGGAGAAGCGAGGCCCCAGGCGC 224

Db        125 GGCGTGGAGTTCCTGCCAGTCAACAACGTCAAGAAGGTGGAAAAGCATGGCCCGGGGCGC 184

Qy        225 TGGGTGGTGCTGGTGGCAGTGCTGTTCAGCTTCCTCTTGCTCTCCCTCATGGCTGGCTTG 284

Db        185 TGGGTGGTGCTGGCAGCCGTGCTGATCGGCCTCCTCTTGGTCTTGCTGGGGATCGGCTTC 244

Qy        285 CTGGTGTGGCACTTCCATTATCGGAATGTGCGGGTTCAAAAAGTCTTCAATGGCCATCTG 344

Db        245 CTGGTGTGGCATTTGCAGTACCGGGACGTGCGTGTCCAGAAGGTCTTCAATGGCTACATG 304

Qy        345 AGGATCACAAATGAGATCTTTCTGGATGCGTATGAGAACTCCACCTCCACAGAGTTTATC 404

Db        305 AGGATCACAAATGAGAATTTTGTGGATGCCTACGAGAACTCCAACTCCACTGAGTTTGTA 364

Qy        405 AGCCTGGCCAGCCAGGTGAAGGAGGCGCTGAAGCTGCTGTACAATGAAGTCCCTGTCCTG 464

Db        365 AGCCTGGCCAGCAAGGTGAAGGACGCGCTGAAGCTGCTGTACAGCGGAGTCCCATTCCTG 424

Qy        465 GGTCCCTACCACAAGAAGTCGGCTGTAACTGCCTTCAGTGAGGGCAGTGTCATCGCCTAC 524

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Qy        525 TACTGGTCAGAGTTCAGCATCCCCCCACACCTGGCAGAAGAGGTTGATCGCGCCATGGCT 584

Db        485 TACTGGTCTGAGTTCAGCATCCCGCAGCACCTGGTGGAGGAGGCCGAGCGCGTCATGGCC 544

Qy        585 GTGGAGCGAGTTGTAACATTGCCACCCCGAGCACGGGCACTGAAATCCTTCGTGCTAACA 644

Db        545 GAGGAGCGCGTAGTCATGCTGCCCCCGCGGGCGCGCTCCCTGAAGTCCTTTGTGGTCACC 604

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Db        785 GTGCTGAGCCTCACCTTCCGCAGCTTTGACCTTGCGTCCTGCGACGAGCGCGGCAGCGAC 844

Qy        885 CTGGTCACCGTGTATGATAGCCTGAGCCCCATGGAACCCCACGCTGTGGTGCGGCTGTGT 944

Db        845 CTGGTGACGGTGTACAACACCCTGAGCCCCATGGAGCCCCACGCCCTGGTGCAGTTGTGT 904

Qy        945 GGCACCTTCTCACCCTCCTACAACCTGACTTTCCTCTCCTCCCAGAACGTCTTCCTTGTC 1004

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Db        965 ACACTGATAACCAACACTGAGCGGCGGCATCCCGGCTTTGAGGCCACCTTCTTCCAGCTG 1024

Qy       1065 CCCAAGATGAGCAGCTGTGGCGGCTTTTTGAGTGACACCCAAGGGACATTTAGCAGCCCC 1124

Db       1025 CCTAGGATGAGCAGCTGTGGAGGCCGCTTACGTAAAGCCCAGGGGACATTCAACAGCCCC 1084

Qy       1125 TACTATCCAGGCCACTACCCGCCCAACATCAACTGCACATGGAATATCAAGGTGCCCAAC 1184

Db       1085 TACTACCCAGGCCACTACCCACCCAACATTGACTGCACATGGAACATTGAGGTGCCCAAC 1144

Qy       1185 AACCGGAACGTGAAGGTGCGCTTCAAACTCTTCTATCTGGTGGACCCCAACGTACCAGTG 1244

Db       1145 AACCAGCATGTGAAGGTGAGCTTCAAATTCTTCTACCTGCTGGAGCCCGGCGTGCCTGCG 1204

Qy       1245 GGCTCCTGCACCAAGGACTATGTGGAGATCAACGGGGAGAAGTACTGCGGTGAGAGGTCC 1304

Db       1205 GGCACCTGCCCCAAGGACTACGTGGAGATCAATGGGGAGAAATACTGCGGAGAGAGGTCC 1264

Qy       1305 CAGTTTGTGGTGAGCAGCAACAGCAGCAAGATTACAGTCCACTTCCATTCTGATCACTCG 1364

Db       1265 CAGTTCGTCGTCACCAGCAACAGCAACAAGATCACAGTTCGCTTCCACTCAGATCAGTCC 1324
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Qy       1365 TACACGGACACCGGGTTCCTAGCTGAGTACCTCTCCTACGACTCCAACGACCCGTGCCCA 1424
             ||||| |||||||| ||| ||||||| ||||||||||||||||||||  ||||| |||||
Db       1325 TACACCGACACCGGCTTCTTAGCTGAATACCTCTCCTACGACTCCAGTGACCCATGCCCG 1384

Qy       1425 GGGATGTTCATGTGCAAGACTGGACGGTGCATCCGAAAGGAACTGCGCTGCGACGGCTGG 1484
             |||  ||||| |||    || || ||||| ||||| ||||| |||||||| || ||||||
Db       1385 GGGCAGTTCACGTGCCGCACGGGGCGGTGTATCCGGAAGGAGCTGCGCTGTGATGGCTGG 1444

Qy       1485 GCAGACTGCCCGGATTATAGTGATGAGCGTTACTGCCGATGCAATGCCACCCACCAGTTC 1544
             || |||||| | ||  | || |||||||    |||||  | |||  | |||  ||||||||||
Db       1445 GCCGACTGCACCGACCACAGCGATGAGCTCAACTGCAGTTGCGACGCCGGCCACCAGTTC 1504

Qy       1545 ACGTGCAAAAACCAGTTCTGCAAGCCCCTCTTCTGGGTCTGTGACAGTGTCAACGACTGT 1604
             |||||||| ||| |||||||||||||||||||||||||||| ||||||||  ||||||||
Db       1505 ACGTGCAAGAACAAGTTCTGCAAGCCCCTCTTCTGGGTCTGCGACAGTGTGAACGACTGC 1564

Qy       1605 GGGGACGGAAGTGACGAGGAGGGCTGCAGCTGTCCTGCTGGGAGTTTCAAGTGTTCCAAT 1664
             || |||  || ||||||  |||| ||||| ||||| ||    ||  |||| ||||||||||
Db       1565 GGAGACAACAGCGACGAGCAGGGGTGCAGTTGTCCGGCCCAGACCTTCAGGTGTTCCAAT 1624

Qy       1665 GGGAAGTGTCTCCCTCAGAGCCAGAAGTGTAATGGGAAGGACAACTGTGGAGATGGGTCT 1724
             |||||||| ||| |  | |||||| |||| |||||||||||| |||||||  || |||||
Db       1625 GGGAAGTGCCTCTCGAAAAGCCAGCAGTGCAATGGGAAGGACGACTGTGGGGACGGGTCC 1684

Qy       1725 GACGAGGCTTCATGTGACAGCGTGAATGTCGTCTCTTGCACCAAATATACCTACCGCTGC 1784
             |||||||| || ||   ||  ||||| |||||| |||| |||||| | ||||||||||||
Db       1685 GACGAGGCCTCCTGCCCCAAGGTGAACGTCGTCACTTGTACCAAACACACCTACCGCTGC 1744

Qy       1785 CAAAATGGCCTCTGTCTGAGCAAGGGCAACCCTGAGTGTGATGGGAAGACGGACTGTAGC 1844
             |  ||||| |||||  |||||||||||||||||||||||||||||| ||||||  ||||||||
Db       1745 CTCAATGGGCTCTGCTTGAGCAAGGGCAACCCTGAGTGTGACGGGAAGGAGGACTGTAGC 1804

Qy       1845 GATGGCTCCGATGAGAAAAACTGTGACTGTGGGCTGCGATCCTTTACCAAACAGGCTCGC 1904
             || ||||| |||||||||  |||| |||||||||||||| || || || | |||||||||
Db       1805 GACGGCTCAGATGAGAAGGACTGCGACTGTGGGCTGCGGTCATTCACGAGACAGGCTCGT 1864

Qy       1905 GTGGTTGGTGGCACGAATGCGGACGAGGGCGAGTGGCCCTGGCAGGTGAGCCTCCACGCC 1964
             || ||||| |||||| ||||||| |||||||||||||||||||||| ||||| || ||
Db       1865 GTTGTTGGGGGCACGGATGCGGATGAGGGCGAGTGGCCCTGGCAGGTAAGCCTGCATGCT 1924

Qy       1965 CTGGGCCAGGGCCACTTGTGTGGGGCCTCGCTCATCTCTCCTGACTGGCTGGTCTCTGCA 2024
             |||||||||||||| | || || || |||||||||||  ||||||||||||||||||||
Db       1925 CTGGGCCAGGGCCACATCTGCGGTGCTTCCCTCATCTCTCCCAACTGGCTGGTCTCTGCC 1984

Qy       2025 GCTCATTGCTTTCAGGATGACAAAAATTTCAAGTACTCAGACTACACGATGTGGACGGCC 2084
             || || ||||      |||||| |  |||| |||||||||||  ||||  ||||||||||
Db       1985 GCACACTGCTACATCGATGACAGAGGATTCAGGTACTCAGACCCCACGCAGTGGACGGCC 2044

Qy       2085 TTCCTGGGTCTGCTGGACCAGAGCAAGCGCAGTGCCTCTGGGGTGCAGGAGCTGAAGCTC 2144
             ||||||||  ||| |||||||| |||||| ||| ||||||||||||||  | ||||
Db       2045 TTCCTGGGCTTGCACGACCAGAGCCAGCGCAGCGCCCCTGGGGTGCAGGAGCGCAGGCTC 2104

Qy       2145 AAACGTATCATCACCCACCCTTCCTTCAATGATTTCACCTTCGACTATGACATCGCCTTG 2204
             || || |||||| |||||| | |||||||| |||||||||||||||||||||||||||  ||
Db       2105 AAGCGCATCATCTCCCACCCCTTCTTCAATGACTTCACCTTCGACTATGACATCGCGCTG 2164

Qy       2205 CTGGAGCTGGAGAAGTCGGTGGAGTACAGCACCGTCGTGCGCCCCATCTGCCTGCCTGAT 2264
             |||||||||||||  |||  |||||||| || | |||||  |||||||||||||||  ||
Db       2165 CTGGAGCTGGAGAAACCGGCAGAGTACAGCTCCATGGTGCGGCCCATCTGCCTGCCGGAC 2224

Qy       2265 GCTACCCATGTCTTCCCTGCTGGCAAGGCCATCTGGGTCACAGGCTGGGGGCACACAAAA 2324
             ||  |||||||||||||| |||||||||||||||||||| |||||||  |||||  |
Db       2225 GCCTCCCATGTCTTCCCTGCCGGCAAGGCCATCTGGGTCACGGGCTGGGGACACACCCAG 2284

Qy       2325 GAGGGAGGTACCGGAGCGCTGATCCTGCAGAAGGGTGAGATCCGTGTCATCAACCAGACC 2384
             | ||||| || || |||||||||||||| |||||||||||||| ||||||||||||||||||
Db       2285 TATGGAGGCACTGGCGCGCTGATCCTGCAAAAGGGTGAGATCCGCGTCATCAACCAGACC 2344

Qy       2385 ACCTGTGAGGACCTCATGCCGCAGCAGATCACCCCACGAATGATGTGTGTGGGTTTCCTC 2444
             ||||| ||| ||||| |||||||||||||||| || || |||||||| ||||| ||||||
Db       2345 ACCTGCGAGAACCTCCTGCCGCAGCAGATCACGCCGCGCATGATGTGCGTGGGCTTCCTC 2404

Qy       2445 AGTGGGGGTGTGGACTCCTGCCAGGGTGACTCTGGTGGCCCCTTGTCAAGCGCGGAGAAA 2504
             || || || |||||||||||||||||||||||||| || || || ||| |||| |||| ||||
Db       2405 AGCGGCGGCGTGGACTCCTGCCAGGGTGATTCCGGGGGACCCCTGTCCAGCGTGGAGGCG 2464

Qy       2505 GATGGGCGAATGTTCCAGGCTGGTGTGGTGAGCTGGGGTGAAGGCTGCGCTCAGAGGAAC 2564
             |||||||| || |||||||| |||||||||||||||||| || ||||||||||||||||||
Db       2465 GATGGGCGGATCTTCCAGGCCGGTGTGGTGAGCTGGGGAGACGGCTGCGCTCAGAGGAAC 2524

Qy       2565 AAGCCAGGCGTGTACACAAGGCTCCCTGTAGTTCGGGACTGGATCAAAGAGCACACTGGG 2624
             |||||||||||||||||||||||||||||| | ||||||||||||||||||| ||||||||
Db       2525 AAGCCAGGCGTGTACACAAGGCTCCCTCTGTTTCGGGACTGGATCAAAGAGAACACTGGG 2584

Qy       2625 GTATAGCAGCATGGACAGACAGCCGACCACAAACACCCACAGGGATGCCCGACATGCACA 2684
             ||||||  ||  ||   | || || |     |||||  | |||   |||  | | |||
Db       2585 GTATAGGGGCCGGG---GCCACCCAAATGTGTACACCTGCGGGGCCACCCATCGTCCACC 2641

Qy       2685 CCTGGATACAGGAGAGGAACACTGACGACATTTATGCTGTGGCCTCCCCCCCCCAACACA 2744
             || |  | || |    | |  |||  |||       ||||    | ||  | |||  || |
Db       2642 CCAGTGTGCACG-CCTGCAGGCTGGAGACTGGACCGCTGACTGCACCAGCGCCC-CCAGA 2699

Qy       2745 ACCCAGACTGTGAACTGCATCCTTAGGACTCAGAGT 2780
             ||  | ||||||||||  |||   ||| |||  | |
Db       2700 ACATACACTGTGAACTCAATCTCCAGGGCTCCAAAT 2735


RESULT 8
US-10-190-030B-1
; Sequence 1, Application US/10190030B
; Publication No. US20030134298A1
; GENERAL INFORMATION:
;  APPLICANT: Madison, Edwin
;  APPLICANT:  Ong, Edgar
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING A
;  TITLE OF INVENTION:  TRANSMEMBRANE SERINE PROTEASE 20, THE ENCODED POLYPEPTIDES AND
;  TITLE OF INVENTION:  METHODS BASED THEREON
;  FILE REFERENCE: 24745-1618
;  CURRENT APPLICATION NUMBER: US/10/190,030B
;  CURRENT FILING DATE:  2002-07-03
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 3147
;   TYPE: DNA
;   ORGANISM: Homo Sapien
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (23)...(2589)
;   OTHER INFORMATION: Nucleotide sequence encoding MTSP1
;  PUBLICATION INFORMATION:
;   AUTHORS: O'Brien, T.J. and Tanimoto, H.
;   DATABASE ACCESSION NUMBER: GenBank #AR081724
;   DATABASE ENTRY DATE: 2000-08-31
;   PATENT DOCUMENT NUMBER: 5,972,616
;   PATENT FILING DATE: 1998-02-20
;   PUBLICATION DATE: 1999-10-26
US-10-190-030B-1

  Query Match           60.6%;  Score 1883.2;  DB 13;  Length 3147;
  Best Local Similarity   81.2%;  Pred. No. 0;
  Matches 2223;  Conservative    0;  Mismatches  508;  Indels    5;  Gaps    3;

Qy         45 GATCGGACCGCCAAAACCATGGGTAGCAATCGGGGCCGCAAGGCCGGAGGGGGCTCTCAG 104
              || ||| |       |||||||| ||| |||||| |||||||| |||||||||  |  ||
Db          5 GAGCGGCCTCGGGGTACCATGGGGAGCGATCGGGCCCGCAAGGGCGGAGGGGGCCCGAAG 64

Qy        105 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCTAGAGAACATGAATGGCTTTGAGGAG 164
              |||||||||||||||||||||||||||||||||||||||||||||  |||||  |||||||||
Db         65 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCACGAGAAAGTGAATGGCTTGGAGGAA 124

Qy        165 GGTGTGGAGTTCCTGCCTGCGAACAATGCCAAGAAAGTGGAGAAGCGAGGCCCCAGGCGC 224
              || |||||||||||||  |||||  | ||||||  |||||  ||||  |||||  |||||
Db        125 GGCGTGGAGTTCCTGCCAGTCAACAACGTCAAGAAGGTGGAAAAGCATGGCCCGGGGCGC 184
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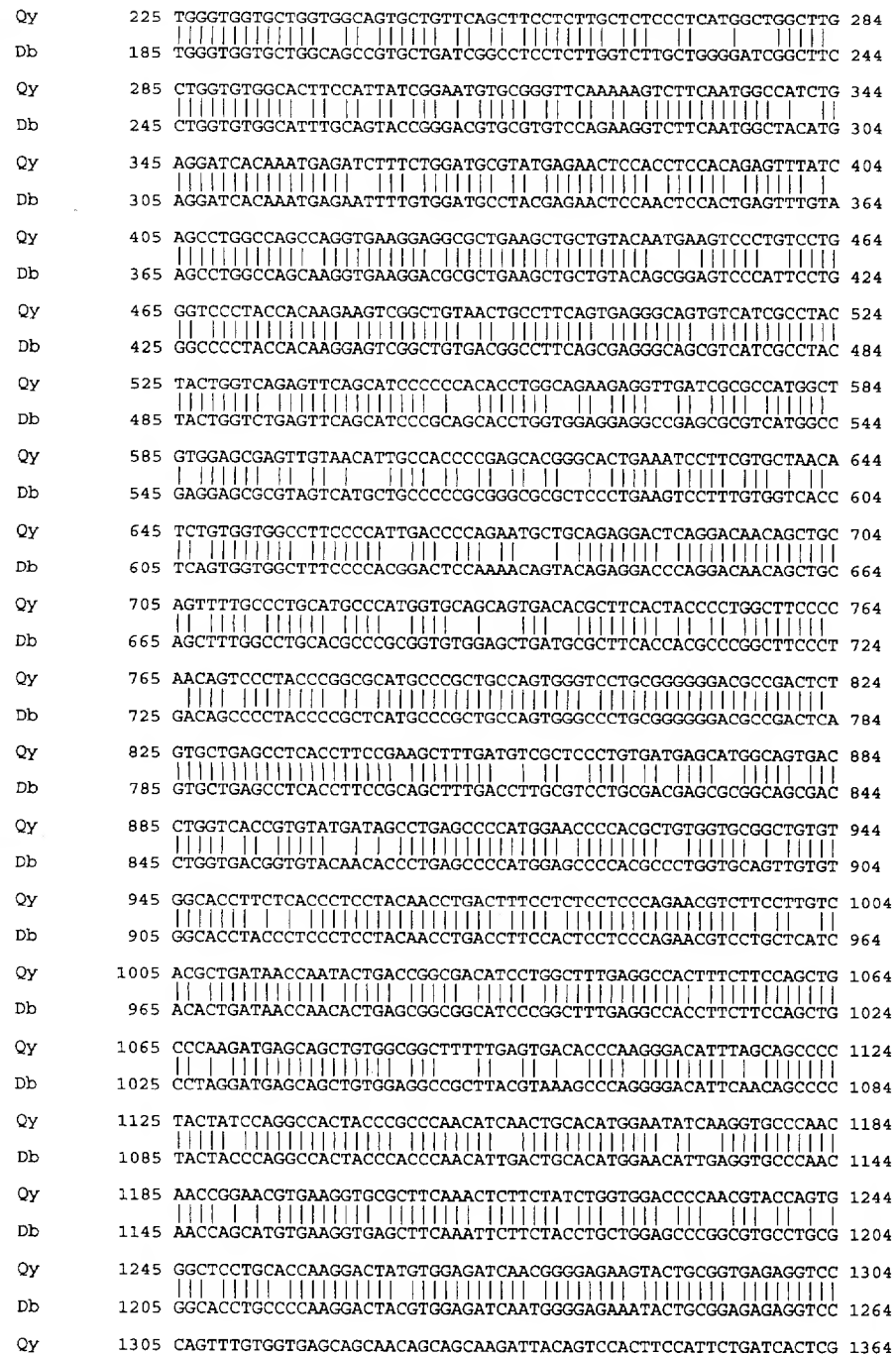
Qy 225 TGGGTGGTGCTGGTGGCAGTGCTGTTCAGCTTCCTCTTGCTCTCCCTCATGGCTGGCTTG 284
Db 185 TGGGTGGTGCTGGCAGCCGTGCTGATCGGCCTCCTCTTGGTCTTGCTGGGGATCGGCTTC 244
Qy 285 CTGGTGTGGCACTTCCATTATCGGAATGTGCGGGTTCAAAAAGTCTTCAATGGCCATCTG 344
Db 245 CTGGTGTGGCATTTGCAGTACCGGGACGTGCGTGTCCAGAAGGTCTTCAATGGCTACATG 304
Qy 345 AGGATCACAAATGAGATCTTTCTGGATGCGTATGAGAACTCCACCTCCACAGAGTTTATC 404
Db 305 AGGATCACAAATGAGAATTTTGTGGATGCCTACGAGAACTCCAACTCCACTGAGTTTGTA 364
Qy 405 AGCCTGGCCAGCCAGGTGAAGGAGGCGCTGAAGCTGCTGTACAATGAAGTCCCTGTCCTG 464
Db 365 AGCCTGGCCAGCAAGGTGAAGGACGCGCTGAAGCTGCTGTACAGCGGAGTCCCATTCCTG 424
Qy 465 GGTCCCTACCACAAGAAGTCGGCTGTAACTGCCTTCAGTGAGGGCAGTGTCATCGCCTAC 524
Db 425 GGCCCCTACCACAAGGAGTCGGCTGTGACGGCCTTCAGCGAGGGCAGCGTCATCGCCTAC 484
Qy 525 TACTGGTCAGAGTTCAGCATCCCCCCACACCTGGCAGAAGAGGTTGATCGCGCCATGGCT 584
Db 485 TACTGGTCTGAGTTCAGCATCCCGCAGCACCTGGTGGAGGAGGCCGAGCGCGTCATGGCC 544
Qy 585 GTGGAGCGAGTTGTAACATTGCCACCCCGAGCACGGGCACTGAAATCCTTCGTGCTAACA 644
Db 545 GAGGAGCGCGTAGTCATGCTGCCCCCGCGGGCGCGCTCCCTGAAGTCCTTTGTGGTCACC 604
Qy 645 TCTGTGGTGGCCTTCCCCATTGACCCCAGAATGCTGCAGAGGACTCAGGACAACAGCTGC 704
Db 605 TCAGTGGTGGCTTTCCCCACGGACTCCAAAACAGTACAGAGGACCCAGGACAACAGCTGC 664
Qy 705 AGTTTTGCCCTGCATGCCCATGGTGCAGCAGTGACACGCTTCACTACCCCTGGCTTCCCC 764
Db 665 AGCTTTGGCCTGCACGCCCGCGGTGTGGAGCTGATGCGCTTCACCACGCCCGGCTTCCCT 724
Qy 765 AACAGTCCCTACCCGGCGCATGCCCGCTGCCAGTGGGTCCTGCGGGGGGACGCCGACTCT 824
Db 725 GACAGCCCCTACCCCGCTCATGCCCGCTGCCAGTGGGCCCTGCGGGGGGACGCCGACTCA 784
Qy 825 GTGCTGAGCCTCACCTTCCGAAGCTTTGATGTCGCTCCCTGTGATGAGCATGGCAGTGAC 884
Db 785 GTGCTGAGCCTCACCTTCCGCAGCTTTGACCTTGCGTCCTGCGACGAGCGCGGCAGCGAC 844
Qy 885 CTGGTCACCGTGTATGATAGCCTGAGCCCCATGGAACCCCACGCTGTGGTGCGGCTGTGT 944
Db 845 CTGGTGACGGTGTACAACACCCTGAGCCCCATGGAGCCCCACGCCCTGGTGCAGTTGTGT 904
Qy 945 GGCACCTTCTCACCCTCCTACAACCTGACTTTCCTCTCCTCCCAGAACGTCTTCCTTGTC 1004
Db 905 GGCACCTACCCTCCCTCCTACAACCTGACCTTCCACTCCTCCCAGAACGTCCTGCTCATC 964
Qy 1005 ACGCTGATAACCAATACTGACCGGCGACATCCTGGCTTTGAGGCCACTTTCTTCCAGCTG 1064
Db 965 ACACTGATAACCAACACTGAGCGGCGGCATCCCGGCTTTGAGGCCACCTTCTTCCAGCTG 1024
Qy 1065 CCCAAGATGAGCAGCTGTGGCGGCTTTTTGAGTGACACCCAAGGGACATTTAGCAGCCCC 1124
Db 1025 CCTAGGATGAGCAGCTGTGGAGGCCGCTTACGTAAAGCCCAGGGGACATTCAACAGCCCC 1084
Qy 1125 TACTATCCAGGCCACTACCCGCCCAACATCAACTGCACATGGAATATCAAGGTGCCCAAC 1184
Db 1085 TACTACCCAGGCCACTACCCACCCAACATTGACTGCACATGGAACATTGAGGTGCCCAAC 1144
Qy 1185 AACCGGAACGTGAAGGTGCGCTTCAAACTCTTCTATCTGGTGGACCCCAACGTACCAGTG 1244
Db 1145 AACCAGCATGTGAAGGTGAGCTTCAAATTCTTCTACCTGCTGGAGCCCGGCGTGCCTGCG 1204
Qy 1245 GGCTCCTGCACCAAGGACTATGTGGAGATCAACGGGGAGAAGTACTGCGGTGAGAGGTCC 1304
Db 1205 GGCACCTGCCCCAAGGACTACGTGGAGATCAATGGGGAGAAATACTGCGGAGAGAGGTCC 1264
Qy 1305 CAGTTTGTGGTGAGCAGCAACAGCAGCAAGATTACAGTCCACTTCCATTCTGATCACTCG 1364
Db 1265 CAGTTCGTCGTCACCAGCAACAGCAACAAGATCACAGTTCGCTTCCACTCAGATCAGTCC 1324
Qy 1365 TACACGGACACCGGGTTCCTAGCTGAGTACCTCTCCTACGACTCCAACGACCCGTGCCCA 1424
Db 1325 TACACCGACACCGGCTTCTTAGCTGAATACCTCTCCTACGACTCCAGTGACCCATGCCCG 1384
Qy 1425 GGGATGTTCATGTGCAAGACTGGACGGTGCATCCGAAAGGAACTGCGCTGCGACGGCTGG 1484
Db 1385 GGGCAGTTCACGTGCCGCACGGGGCGGTGTATCCGGAAGGAGCTGCGCTGTGATGGCTGG 1444
Qy 1485 GCAGACTGCCCGGATTATAGTGATGAGCGTTACTGCCGATGCAATGCCACCCACCAGTTC 1544
Db 1445 GCCGACTGCACCGACCACAGCGATGAGCTCAACTGCAGTTGCGACGCCGGCCACCAGTTC 1504
Qy 1545 ACGTGCAAAAACCAGTTCTGCAAGCCCCTCTTCTGGGTCTGTGACAGTGTCAACGACTGT 1604
Db 1505 ACGTGCAAGAACAAGTTCTGCAAGCCCCTCTTCTGGGTCTGCGACAGTGTGAACGACTGC 1564
Qy 1605 GGGGACGGAAGTGACGAGGAGGGCTGCAGCTGTCCTGCTGGGAGTTTCAAGTGTTCCAAT 1664
Db 1565 GGAGACAACAGCGACGAGCAGGGGTGCAGTTGTCCGGCCCAGACCTTCAGGTGTTCCAAT 1624
Qy 1665 GGGAAGTGTCTCCCTCAGAGCCAGAAGTGTAATGGGAAGGACAACTGTGGAGATGGGTCT 1724
Db 1625 GGGAAGTGCCTCTCGAAAAGCCAGCAGTGCAATGGGAAGGACGACTGTGGGGACGGGTCC 1684
Qy 1725 GACGAGGCTTCATGTGACAGCGTGAATGTCGTCTCTTGCACCAAATATACCTACCGCTGC 1784
Db 1685 GACGAGGCCTCCTGCCCCAAGGTGAACGTCGTCACTTGTACCAAACACACCTACCGCTGC 1744
Qy 1785 CAAAATGGCCTCTGTCTGAGCAAGGGCAACCCTGAGTGTGATGGGAAGACGGACTGTAGC 1844
Db 1745 CTCAATGGGCTCTGCTTGAGCAAGGGCAACCCTGAGTGTGACGGGAAGGAGGACTGTAGC 1804
Qy 1845 GATGGCTCCGATGAGAAAAACTGTGACTGTGGGCTGCGATCCTTTACCAAACAGGCTCGC 1904
Db 1805 GACGGCTCAGATGAGAAGGACTGCGACTGTGGGCTGCGGTCATTCACGAGACAGGCTCGT 1864
Qy 1905 GTGGTTGGTGGCACGAATGCGGACGAGGGCGAGTGGCCCTGGCAGGTGAGCCTCCACGCC 1964
Db 1865 GTTGTTGGGGGCACGGATGCGGATGAGGGCGAGTGGCCCTGGCAGGTAAGCCTGCATGCT 1924
Qy 1965 CTGGGCCAGGGCCACTTGTGTGGGGCCTCGCTCATCTCTCCTGACTGGCTGGTCTCTGCA 2024
Db 1925 CTGGGCCAGGGCCACATCTGCGGTGCTTCCCTCATCTCTCCCAACTGGCTGGTCTCTGCC 1984
Qy 2025 GCTCATTGCTTTCAGGATGACAAAAATTTCAAGTACTCAGACTACACGATGTGGACGGCC 2084
Db 1985 GCACACTGCTACATCGATGACAGAGGATTCAGGTACTCAGACCCCACGCAGTGGACGGCC 2044
Qy 2085 TTCCTGGGTCTGCTGGACCAGAGCAAGCGCAGTGCCTCTGGGGTGCAGGAGCTGAAGCTC 2144
Db 2045 TTCCTGGGCTTGCACGACCAGAGCCAGCGCAGCGCCCCTGGGGTGCAGGAGCGCAGGCTC 2104
Qy 2145 AAACGTATCATCACCCACCCTTCCTTCAATGATTTCACCTTCGACTATGACATCGCCTTG 2204
Db 2105 AAGCGCATCATCTCCCACCCCTTCTTCAATGACTTCACCTTCGACTATGACATCGCGCTG 2164
Qy 2205 CTGGAGCTGGAGAAGTCGGTGGAGTACAGCACCGTCGTGCGCCCCATCTGCCTGCCTGAT 2264
Db 2165 CTGGAGCTGGAGAAACCGGCAGAGTACAGCTCCATGGTGCGGCCCATCTGCCTGCCGGAC 2224
Qy 2265 GCTACCCATGTCTTCCCTGCTGGCAAGGCCATCTGGGTCACAGGCTGGGGGCACACAAAA 2324
Db 2225 GCCTCCCATGTCTTCCCTGCCGGCAAGGCCATCTGGGTCACGGGCTGGGGACACACCCAG 2284
Qy 2325 GAGGGAGGTACCGGAGCGCTGATCCTGCAGAAGGGTGAGATCCGTGTCATCAACCAGACC 2384
Db 2285 TATGGAGGCACTGGCGCGCTGATCCTGCAAAAGGGTGAGATCCGCGTCATCAACCAGACC 2344
Qy 2385 ACCTGTGAGGACCTCATGCCGCAGCAGATCACCCCACGAATGATGTGTGTGGGTTTCCTC 2444

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Db       2345 ACCTGCGAGAACCTCCTGCCGCAGCAGATCACGCCGCGCATGATGTGCGTGGGCTTCCTC 2404

Qy       2445 AGTGGGGGTGTGGACTCCTGCCAGGGTGACTCTGGTGGCCCCCTTGTCAAGCGCGGAGAAA 2504

Db       2405 AGCGGCGGCGTGGACTCCTGCCAGGGTGATTCCGGGGGACCCCTGTCCAGCGTGGAGGCG 2464

Qy       2505 GATGGGCGAATGTTCCAGGCTGGTGTGGTGAGCTGGGGTGAAGGCTGCGCTCAGAGGAAC 2564

Db       2465 GATGGGCGGATCTTCCAGGCCGGTGTGGTGAGCTGGGGAGACGGCTGCGCTCAGAGGAAC 2524

Qy       2565 AAGCCAGGCGTGTACACAAGGCTCCCTGTAGTTCGGGACTGGATCAAAGAGCACACTGGG 2624

Db       2525 AAGCCAGGCGTGTACACAAGGCTCCCTCTGTTTCGGGACTGGATCAAAGAGAACACTGGG 2584

Qy       2625 GTATAGCAGCATGGACAGACAGCCGACCACAAACACCCACAGGGATGCCCGACATGCACA 2684

Db       2585 GTATAGGGGCCGGG---GCCACCCAAATGTGTACACCTGCGGGGCCACCCATCGTCCACC 2641

Qy       2685 CCTGGATACAGGAGAGGAACACTGACGACATTTATGCTGTGGCCTCCCCCCCCCAACACA 2744

Db       2642 CCAGTGTGCACG-CCTGCAGGCTGGAGACTGGACCGCTGACTGCACCAGCGCCC-CCAGA 2699

Qy       2745 ACCCAGACTGTGAACTGCATCCTTAGGACTCAGAGT 2780

Db       2700 ACATACACTGTGAACTCAATCTCCAGGGCTCCAAAT 2735


RESULT 9
US-10-190-030B-3
; Sequence 3, Application US/10190030B
; Publication No. US20030134298A1
; GENERAL INFORMATION:
;  APPLICANT: Madison, Edwin
;  APPLICANT:  Ong, Edgar
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING A
;  TITLE OF INVENTION:  TRANSMEMBRANE SERINE PROTEASE 20, THE ENCODED POLYPEPTIDES AND
;  TITLE OF INVENTION:  METHODS BASED THEREON
;  FILE REFERENCE: 24745-1618
;  CURRENT APPLICATION NUMBER: US/10/190,030B
;  CURRENT FILING DATE:  2002-07-03
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 3147
;   TYPE: DNA
;   ORGANISM: Homo Sapien
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1865)...(2590)
;   OTHER INFORMATION: Nucleic acid sequence of protease domain of MTSP1
US-10-190-030B-3

  Query Match             60.6%;  Score 1883.2;  DB 13;  Length 3147;
  Best Local Similarity   81.2%;  Pred. No. 0;
  Matches 2223;  Conservative    0;  Mismatches  508;  Indels    5;  Gaps    3;

Qy         45 GATCGGACCGCCAAAACCATGGGTAGCAATCGGGGCCGCAAGGCCGGAGGGGGCTCTCAG 104

Db          5 GAGCGGCCTCGGGGTACCATGGGGAGCGATCGGGCCCGCAAGGGCGGAGGGGGCCCGAAG 64

Qy        105 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCTAGAGAACATGAATGGCTTTGAGGAG 164

Db         65 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCACGAGAAAGTGAATGGCTTGGAGGAA 124

Qy        165 GGTGTGGAGTTCCTGCCTGCGAACAATGCCAAGAAAGTGGAGAAGCGAGGCCCCAGGCGC 224

Db        125 GGCGTGGAGTTCCTGCCAGTCAACAACGTCAAGAAGGTGGAAAAGCATGGCCCGGGGCGC 184

Qy        225 TGGGTGGTGCTGGTGGCAGTGCTGTTCAGCTTCCTCTTGCTCTCCCTCATGGCTGGCTTG 284

Db        185 TGGGTGGTGCTGGCAGCCGTGCTGATCGGCCTCCTCTTGGTCTTGCTGGGGATCGGCTTC 244

Qy        285 CTGGTGTGGCACTTCCATTATCGGAATGTGCGGGTTCAAAAAGTCTTCAATGGCCATCTG 344

Db        245 CTGGTGTGGCATTTGCAGTACCGGGACGTGCGTGTCCAGAAGGTCTTCAATGGCTACATG 304

Qy        345 AGGATCACAAATGAGATCTTTCTGGATGCGTATGAGAACTCCACCTCCACAGAGTTTATC 404

Db        305 AGGATCACAAATGAGAATTTTGTGGATGCCTACGAGAACTCCAACTCCACTGAGTTTGTA 364

Qy        405 AGCCTGGCCAGCCAGGTGAAGGAGGCGCTGAAGCTGCTGTACAATGAAGTCCCTGTCCTG 464

Db        365 AGCCTGGCCAGCAAGGTGAAGGACGCGCTGAAGCTGCTGTACAGCGGAGTCCCATTCCTG 424

Qy        465 GGTCCCTACCACAAGAAGTCGGCTGTAACTGCCTTCAGTGAGGGCAGTGTCATCGCCTAC 524

Db        425 GGCCCCTACCACAAGGAGTCGGCTGTGACGGCCTTCAGCGAGGGCAGCGTCATCGCCTAC 484

Qy        525 TACTGGTCAGAGTTCAGCATCCCCCCACACCTGGCAGAAGAGGTTGATCGCGCCATGGCT 584

Db        485 TACTGGTCTGAGTTCAGCATCCCGCAGCACCTGGTGGAGGAGGCCGAGCGCGTCATGGCC 544

Qy        585 GTGGAGCGAGTTGTAACATTGCCACCCCGAGCACGGGCACTGAAATCCTTCGTGCTAACA 644

Db        545 GAGGAGCGCGTAGTCATGCTGCCCCCGCGGGCGCGCTCCCTGAAGTCCTTTGTGGTCACC 604

Qy        645 TCTGTGGTGGCCTTCCCCATTGACCCCAGAATGCTGCAGAGGACTCAGGACAACAGCTGC 704

Db        605 TCAGTGGTGGCTTTCCCCACGGACTCCAAAACAGTACAGAGGACCCAGGACAACAGCTGC 664

Qy        705 AGTTTTGCCCTGCATGCCCATGGTGCAGCAGTGACACGCTTCACTACCCCTGGCTTCCCC 764

Db        665 AGCTTTGGCCTGCACGCCCGCGGTGTGGAGCTGATGCGCTTCACCACGCCCGGCTTCCCT 724

Qy        765 AACAGTCCCTACCCGGCGCATGCCCGCTGCCAGTGGGTCCTGCGGGGGGACGCCGACTCT 824

Db        725 GACAGCCCCTACCCCGCTCATGCCCGCTGCCAGTGGGCCCTGCGGGGGGACGCCGACTCA 784

Qy        825 GTGCTGAGCCTCACCTTCCGAAGCTTTGATGTCGCTCCCTGTGATGAGCATGGCAGTGAC 884

Db        785 GTGCTGAGCCTCACCTTCCGCAGCTTTGACCTTGCGTCCTGCGACGAGCGCGGCAGCGAC 844

Qy        885 CTGGTCACCGTGTATGATAGCCTGAGCCCCATGGAACCCCACGCTGTGGTGCGGCTGTGT 944

Db        845 CTGGTGACGGTGTACAACACCCTGAGCCCCATGGAGCCCCACGCCCTGGTGCAGTTGTGT 904

Qy        945 GGCACCTTCTCACCCTCCTACAACCTGACTTTCCTCTCCTCCCAGAACGTCTTCCTTGTC 1004

Db        905 GGCACCTACCCTCCCTCCTACAACCTGACCTTCCACTCCTCCCAGAACGTCCTGCTCATC 964

Qy       1005 ACGCTGATAACCAATACTGACCGGCGACATCCTGGCTTTGAGGCCACTTTCTTCCAGCTG 1064

Db        965 ACACTGATAACCAACACTGAGCGGCGGCATCCCGGCTTTGAGGCCACCTTCTTCCAGCTG 1024

Qy       1065 CCCAAGATGAGCAGCTGTGGCGGCTTTTTGAGTGACACCCAAGGGACATTTAGCAGCCCC 1124

Db       1025 CCTAGGATGAGCAGCTGTGGAGGCCGCTTACGTAAAGCCCAGGGGACATTCAACAGCCCC 1084

Qy       1125 TACTATCCAGGCCACTACCCGCCCAACATCAACTGCACATGGAATATCAAGGTGCCCAAC 1184

Db       1085 TACTACCCAGGCCACTACCCACCCAACATTGACTGCACATGGAACATTGAGGTGCCCAAC 1144

Qy       1185 AACCGGAACGTGAAGGTGCGCTTCAAACTCTTCTATCTGGTGGACCCCAACGTACCAGTG 1244

Db       1145 AACCAGCATGTGAAGGTGAGCTTCAAATTCTTCTACCTGCTGGAGCCCGGCGTGCCTGCG 1204

Qy       1245 GGCTCCTGCACCAAGGACTATGTGGAGATCAACGGGGAGAAGTACTGCGGTGAGAGGTCC 1304

Db       1205 GGCACCTGCCCCAAGGACTACGTGGAGATCAATGGGGAGAAATACTGCGGAGAGAGGTCC 1264

Qy       1305 CAGTTTGTGGTGAGCAGCAACAGCAGCAAGATTACAGTCCACTTCCATTCTGATCACTCG 1364

Db       1265 CAGTTCGTCGTCACCAGCAACAGCAACAAGATCACAGTTCGCTTCCACTCAGATCAGTCC 1324

Qy       1365 TACACGGACACCGGGTTCCTAGCTGAGTACCTCTCCTACGACTCCAACGACCCGTGCCCA 1424
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Db       1325 TACACCGACACCGGCTTCTTAGCTGAATACCTCTCCTACGACTCCAGTGACCCATGCCCG 1384

Qy       1425 GGGATGTTCATGTGCAAGACTGGACGGTGCATCCGAAAGGAACTGCGCTGCGACGGCTGG 1484
             |||  ||||| ||||   || || ||||| ||||| |||||| || ||||||
Db       1385 GGGCAGTTCACGTGCCGCACGGGGCGGTGTATCCGGAAGGAGCTGCGCTGTGATGGCTGG 1444

Qy       1485 GCAGACTGCCCCGGATTATAGTGATGAGCGTTACTGCCGATGCAATGCCACCCACCAGTTC 1544
             || |||||| | ||  | || |||||||   ||||| | ||| | |||  ||||||||||
Db       1445 GCCGACTGCACCGACCACAGCGATGAGCTCAACTGCAGTTGCGACGCCGGCCACCAGTTC 1504

Qy       1545 ACGTGCAAAAACCAGTTCTGCAAGCCCCTCTTCTGGGTCTGTGACAGTGTCAACGACTGT 1604
             |||||||| ||| |||||||||||||||||||||||||||| |||||||| ||||||||
Db       1505 ACGTGCAAGAACAAGTTCTGCAAGCCCCTCTTCTGGGTCTGCGACAGTGTGAACGACTGC 1564

Qy       1605 GGGGACGGAAGTGACGAGGAGGGCTGCAGCTGTCCTGCTGGGAGTTTCAAGTGTTCCAAT 1664
             || ||| || |||||| |||| ||||| ||||| ||   ||  |||| ||||||||||
Db       1565 GGAGACAACAGCGACGAGCAGGGGTGCAGTTGTCCGGCCCAGACCTTCAGGTGTTCCAAT 1624

Qy       1665 GGGAAGTGTCTCCCTCAGAGCCAGAAGTGTAATGGGAAGGACAACTGTGGAGATGGGTCT 1724
             |||||||| ||| |  | |||||| |||| |||||||||||| ||||||| || |||||
Db       1625 GGGAAGTGCCTCTCGAAAAGCCAGCAGTGCAATGGGAAGGACGACTGTGGGGACGGGTCC 1684

Qy       1725 GACGAGGCTTCATGTGACAGCGTGAATGTCGTCTCTTGCACCAAATATACCTACCGCTGC 1784
             |||||||| || ||   || ||||| |||||| |||| |||||| | ||||||||||||
Db       1685 GACGAGGCCTCCTGCCCCAAGGTGAACGTCGTCACTTGTACCAAACACACCTACCGCTGC 1744

Qy       1785 CAAAATGGCCTCTGTCTGAGCAAGGGCAACCCTGAGTGTGATGGGAAGACGGACTGTAGC 1844
             |  ||||| ||||| ||||||||||||||||||||||||||||| ||||||  ||||||||||
Db       1745 CTCAATGGGCTCTGCTTGAGCAAGGGCAACCCTGAGTGTGACGGGAAGGAGGACTGTAGC 1804

Qy       1845 GATGGCTCCGATGAGAAAAACTGTGACTGTGGGCTGCGATCCTTTACCAAACAGGCTCGC 1904
             || ||||| |||||||| |||| ||||||||||||||| || || || | |||||||||
Db       1805 GACGGCTCAGATGAGAAGGACTGCGACTGTGGGCTGCGGTCATTCACGAGACAGGCTCGT 1864

Qy       1905 GTGGTTGGTGGCACGAATGCGGACGAGGGCGAGTGGCCCTGGCAGGTGAGCCTCCACGCC 1964
             || ||||| |||||| ||||||| |||||||||||||||||||||| ||||| || ||
Db       1865 GTTGTTGGGGGCACGGATGCGGATGAGGGCGAGTGGCCCTGGCAGGTAAGCCTGCATGCT 1924

Qy       1965 CTGGGCCAGGGCCACTTGTGTGGGGCCTCGCTCATCTCTCCTGACTGGCTGGTCTCTGCA 2024
             |||||||||||||| | || || || || |||||||||| ||||||||||||||||||
Db       1925 CTGGGCCAGGGCCACATCTGCGGTGCTTCCCTCATCTCTCCCAACTGGCTGGTCTCTGCC 1984

Qy       2025 GCTCATTGCTTTCAGGATGACAAAAATTTCAAGTACTCAGACTACACGATGTGGACGGCC 2084
             || || |||| |||||||| |  |||| |||||||||  ||||  ||||||||||
Db       1985 GCACACTGCTACATCGATGACAGAGGATTCAGGTACTCAGACCCCACGCAGTGGACGGCC 2044

Qy       2085 TTCCTGGGTCTGCTGGACCAGAGCAAGCGCAGTGCCTCTGGGGTGCAGGAGCTGAAGCTC 2144
             |||||||  |||  |||||||| ||||||| ||| |||||||||||||  | ||||
Db       2045 TTCCTGGGCTTGCACGACCAGAGCCAGCGCAGCGCCCCTGGGGTGCAGGAGCGCAGGCTC 2104

Qy       2145 AAACGTATCATCACCCACCCTTCCTTCAATGATTTCACCTTCGACTATGACATCGCCTTG 2204
             || || |||||| ||||||| | |||||||| |||||||||||||||||||||||||  ||
Db       2105 AAGCGCATCATCTCCCACCCCTTCTTCAATGACTTCACCTTCGACTATGACATCGCGCTG 2164

Qy       2205 CTGGAGCTGGAGAAGTCGGTGGAGTACAGCACCGTCGTGCGCCCCATCTGCCTGCCTGAT 2264
             |||||||||||||  |||  |||||||| || | ||||| ||||||||||||||| ||
Db       2165 CTGGAGCTGGAGAAACCGGCAGAGTACAGCTCCATGGTGCGGCCCATCTGCCTGCCGGAC 2224

Qy       2265 GCTACCCATGTCTTCCCTGCTGGCAAGGCCATCTGGGTCACAGGCTGGGGGCACACAAAA 2324
             ||  |||||||||||||| |||||||||||||||||||| |||||||| |||||  |
Db       2225 GCCTCCCATGTCTTCCCTGCCGGCAAGGCCATCTGGGTCACGGGCTGGGGACACACCCAG 2284

Qy       2325 GAGGGAGGTACCGGAGCGCTGATCCTGCAGAAGGGTGAGATCCGTGTCATCAACCAGACC 2384
             | ||||| || ||||||||||||| |||||||||||||| |||||||||||||||||||
Db       2285 TATGGAGGCACTGGCGCGCTGATCCTGCAAAAGGGTGAGATCCGCGTCATCAACCAGACC 2344

Qy       2385 ACCTGTGAGGACCTCATGCCGCAGCAGATCACCCCACGAATGATGTGTGTGGGTTTCCTC 2444
             ||||| ||| ||||| |||||||||||||||| || || |||||||| ||||| ||||||
Db       2345 ACCTGCGAGAACCTCCTGCCGCAGCAGATCACGCCGCGCATGATGTGCGTGGGCTTCCTC 2404

Qy       2445 AGTGGGGGTGTGGACTCCTGCCAGGGTGACTCTGGTGGCCCCTTGTCAAGCGCGGAGAAA 2504
             || || || |||||||||||||||||| || || || ||| |||| |||| ||||
Db       2405 AGCGGCGGCGTGGACTCCTGCCAGGGTGATTCCGGGGGACCCCTGTCCAGCGTGGAGGCG 2464
```

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Qy       2505 GATGGGCGAATGTTCCAGGCTGGTGTGGTGAGCTGGGGTGAAGGCTGCGCTCAGAGGAAC 2564
             |||||||| || |||||||| |||||||||||||||| || ||||||||||||||||||
Db       2465 GATGGGCGGATCTTCCAGGCCGGTGTGGTGAGCTGGGGAGACGGCTGCGCTCAGAGGAAC 2524

Qy       2565 AAGCCAGGCGTGTACACAAGGCTCCCTGTAGTTCGGGACTGGATCAAAGAGCACACTGGG 2624
             |||||||||||||||||||||||||||| | |||||||||||||||||| ||||||||
Db       2525 AAGCCAGGCGTGTACACAAGGCTCCCTCTGTTTCGGGACTGGATCAAAGAGAACACTGGG 2584

Qy       2625 GTATAGCAGCATGGACAGACAGCCGACCACAAACACCCACAGGGATGCCCGACATGCACA 2684
             |||||| ||  ||   | || || |      |||||  | |||   |||  | | |||
Db       2585 GTATAGGGGCCGGG---GCCACCCAAATGTGTACACCTGCGGGGCCACCCATCGTCCACC 2641

Qy       2685 CCTGGATACAGGAGAGGAACACTGACGACATTTATGCTGTGGCCTCCCCCCCCCAACACA 2744
             || |  | || |·   | |  |||  |||      ||||    | ||  | |||  || |
Db       2642 CCAGTGTGCACG-CCTGCAGGCTGGAGACTGGACCGCTGACTGCACCAGCGCCC-CCAGA 2699

Qy       2745 ACCCAGACTGTGAACTGCATCCTTAGGACTCAGAGT 2780
             ||  | ||||||||||  |||   ||| |||  | |
Db       2700 ACATACACTGTGAACTCAATCTCCAGGGCTCCAAAT 2735


RESULT 10
US-10-267-219-1
; Sequence 1, Application US/10267219
; Publication No. US20030143219A1
; GENERAL INFORMATION:
;  APPLICANT: Madison, Edwin
;  APPLICANT:  Yeh, Jiunn-Chern
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING A TRANSMEMBRANE SERINE PROTEASE 2
;  TITLE OF INVENTION:  ENCODED POLYPEPTIDES AND METHODS BASED THEREON
;  FILE REFERENCE: 24745-1621
;  CURRENT APPLICATION NUMBER: US/10/267,219
;  CURRENT FILING DATE:  2002-10-08
;  PRIOR APPLICATION NUMBER: 60/328,530
;  PRIOR FILING DATE: 09-OCT-2001
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 3147
;   TYPE: DNA
;   ORGANISM: Homo Sapien
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (23)...(2589)
;   OTHER INFORMATION: Nucleotide sequence encoding MTSP1
;  PUBLICATION INFORMATION:
;   AUTHORS: O'Brien, T.J. and Tanimoto, H.
;   DATABASE ACCESSION NUMBER: GenBank #AR081724
;   DATABASE ENTRY DATE: 2000-08-31
;   PATENT DOCUMENT NUMBER: 5,972,616
;   PATENT FILING DATE: 1998-02-20
;   PUBLICATION DATE: 1999-10-26
US-10-267-219-1

  Query Match             60.6%;  Score 1883.2;  DB 13;  Length 3147;
  Best Local Similarity   81.2%;  Pred. No. 0;
  Matches 2223;  Conservative    0;  Mismatches  508;  Indels    5;  Gaps    3;

Qy         45 GATCGGACCGCCAAAACCATGGGTAGCAATCGGGGCCGCAAGGCCGGAGGGGGCTCTCAG 104
              || ||| |       |||||||| ||| |||||| |||||||| |||||||||| |  ||
Db          5 GAGCGGCCTCGGGGTACCATGGGGAGCGATCGGGCCCGCAAGGGCGGAGGGGGCCCGAAG 64

Qy        105 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCTAGAGAACATGAATGGCTTTGAGGAG 164
              |||||||||||||||||||||||||||||||| |||||  |||||||||| |||||
Db         65 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCACGAGAAAGTGAATGGCTTGGAGGAA 124

Qy        165 GGTGTGGAGTTCCTGCCTGCGAACAATGCCAAGAAAGTGGAGAAGCGAGGCCCCAGGCGC 224
              || |||||||||||||  |||| | |||||| |||| ||||  |||||  |||||
Db        125 GGCGTGGAGTTCCTGCCAGTCAACAACGTCAAGAAGGTGGAAAAGCATGGCCCGGGGCGC 184

Qy        225 TGGGTGGTGCTGGTGGCAGTGCTGTTCAGCTTCCTCTTGCTCTCCCTCATGGCTGGCTTG 284
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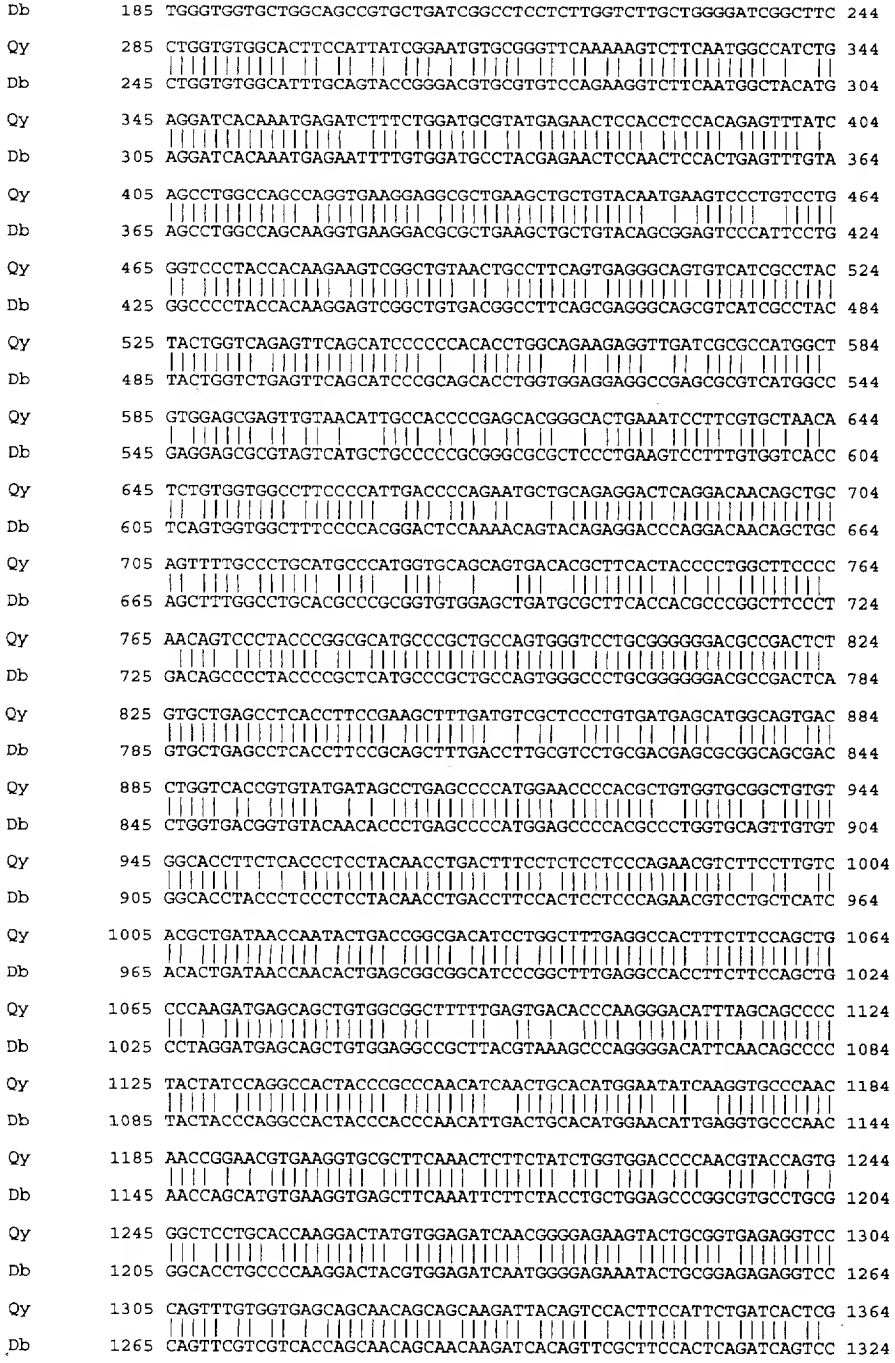
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Db 245 CTGGTGTGGCATTTGCAGTACCGGGACGTGCGTGTCCAGAAGGTCTTCAATGGCTACATG 304
Qy 345 AGGATCACAAATGAGATCTTTCTGGATGCGTATGAGAACTCCACCTCCACAGAGTTTATC 404
Db 305 AGGATCACAAATGAGAATTTTGTGGATGCCTACGAGAACTCCAACTCCACTGAGTTTGTA 364
Qy 405 AGCCTGGCCAGCCAGGTGAAGGAGGCGCTGAAGCTGCTGTACAATGAAGTCCCTGTCCTG 464
Db 365 AGCCTGGCCAGCAAGGTGAAGGACGCGCTGAAGCTGCTGTACAGCGGAGTCCCATTCCTG 424
Qy 465 GGTCCCTACCACAAGAAGTCGGCTGTAACTGCCTTCAGTGAGGGCAGTGTCATCGCCTAC 524
Db 425 GGCCCCTACCACAAGGAGTCGGCTGTGACGGCCTTCAGCGAGGGCAGCGTCATCGCCTAC 484
Qy 525 TACTGGTCAGAGTTCAGCATCCCCCCACACCTGGCAGAAGAGGTTGATCGCGCCATGGCT 584
Db 485 TACTGGTCTGAGTTCAGCATCCCGCAGCACCTGGTGGAGGAGGCCGAGCGCGTCATGGCC 544
Qy 585 GTGGAGCGAGTTGTAACATTGCCACCCCGAGCACGGGCACTGAAATCCTTCGTGCTAACA 644
Db 545 GAGGAGCGCGTAGTCATGCTGCCCCCGCGGGCGCGCTCCCTGAAGTCCTTTGTGGTCACC 604
Qy 645 TCTGTGGTGGCCTTCCCCATTGACCCCAGAATGCTGCAGAGGACTCAGGACAACAGCTGC 704
Db 605 TCAGTGGTGGCTTTCCCCACGGACTCCAAAACAGTACAGAGGACCCAGGACAACAGCTGC 664
Qy 705 AGTTTTGCCCCTGCATGCCCATGGTGCAGCAGTGACACGCTTCACTACCCCTGGCTTCCCC 764
Db 665 AGCTTTGGCCTGCACGCCCGCGGTGTGGAGCTGATGCGCTTCACCACGCCCGGCTTCCCT 724
Qy 765 AACAGTCCCTACCCGGCGCATGCCCGCTGCCAGTGGGTCCTGCGGGGGGACGCCGACTCT 824
Db 725 GACAGCCCCTACCCCGCTCATGCCCGCTGCCAGTGGGCCCTGCGGGGGGACGCCGACTCA 784
Qy 825 GTGCTGAGCCTCACCTTCCGAAGCTTTGATGTCGCTCCCTGTGATGAGCATGGCAGTGAC 884
Db 785 GTGCTGAGCCTCACCTTCCGCAGCTTTGACCTTGCGTCCTGCGACGAGCGCGGCAGCGAC 844
Qy 885 CTGGTCACCGTGTATGATAGCCTGAGCCCCATGGAACCCCACGCTGTGGTGCGGCTGTGT 944
Db 845 CTGGTGACGGTGTACAACACCCTGAGCCCCATGGAGCCCCACGCCCTGGTGCAGTTGTGT 904
Qy 945 GGCACCTTCTCACCCTCCTACAACCTGACTTTCCTCTCCTCCCAGAACGTCTTCCTTGTC 1004
Db 905 GGCACCTACCCTCCCTCCTACAACCTGACCTTCCACTCCTCCCAGAACGTCCTGCTCATC 964
Qy 1005 ACGCTGATAACCAATACTGACCGGCGACATCCTGGCTTTGAGGCCACTTTCTTCCAGCTG 1064
Db 965 ACACTGATAACCAACACTGAGCGGCGGCATCCCGGCTTTGAGGCCACCTTCTTCCAGCTG 1024
Qy 1065 CCCAAGATGAGCAGCTGTGGCGGCTTTTTGAGTGACACCCAAGGGACATTTAGCAGCCCC 1124
Db 1025 CCTAGGATGAGCAGCTGTGGAGGCCGCTTACGTAAAGCCCAGGGGACATTCAACAGCCCC 1084
Qy 1125 TACTATCCAGGCCACTACCCGCCCAACATCAACTGCACATGGAATATCAAGGTGCCCAAC 1184
Db 1085 TACTACCCAGGCCACTACCCACCCAACATTGACTGCACATGGAACATTGAGGTGCCCAAC 1144
Qy 1185 AACCGGAACGTGAAGGTGCGCTTCAAACTCTTCTATCTGGTGGACCCCAACGTACCAGTG 1244
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Db 1205 GGCACCTGCCCCAAGGACTACGTGGAGATCAATGGGGAGAAATACTGCGGAGAGAGGTCC 1264
Qy 1305 CAGTTTGTGGTGAGCAGCAACAGCAGCAAGATTACAGTCCACTTCCATTCTGATCACTCG 1364
Db 1265 CAGTTCGTCGTCACCAGCAACAGCAACAAGATCACAGTTCGCTTCCACTCAGATCAGTCC 1324
Qy 1365 TACACGGACACCGGGTTCCTAGCTGAGTACCTCTCCTACGACTCCAACGACCCGTGCCCA 1424
Db 1325 TACACCGACACCGGCTTCTTAGCTGAATACCTCTCCTACGACTCCAGTGACCCATGCCCG 1384
Qy 1425 GGGATGTTCATGTGCAAGACTGGACGGTGCATCCGAAAGGAACTGCGCTGCGACGGCTGG 1484
Db 1385 GGGCAGTTCACGTGCCGCACGGGGCGGTGTATCCGGAAGGAGCTGCGCTGTGATGGCTGG 1444
Qy 1485 GCAGACTGCCCGGATTATAGTGATGAGCGTTACTGCCGATGCAATGCCACCCACCAGTTC 1544
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Qy 1545 ACGTGCAAAAACCAGTTCTGCAAGCCCCTCTTCTGGGTCTGTGACAGTGTCAACGACTGT 1604
Db 1505 ACGTGCAAGAACAAGTTCTGCAAGCCCCTCTTCTGGGTCTGCGACAGTGTGAACGACTGC 1564
Qy 1605 GGGGACGGAAGTGACGAGGAGGGCTGCAGCTGTCCTGCTGGGAGTTTCAAGTGTTCCAAT 1664
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Qy 1665 GGGAAGTGTCTCCCTCAGAGCCAGAAGTGTAATGGGAAGGACAACTGTGGAGATGGGTCT 1724
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Qy 1725 GACGAGGCTTCATGTGACAGCGTGAATGTCGTCTCTTGCACCAAATATACCTACCGCTGC 1784
Db 1685 GACGAGGCCTCCTGCCCCAAGGTGAACGTCGTCACTTGTACCAAACACACCTACCGCTGC 1744
Qy 1785 CAAAATGGCCTCTGTCTGAGCAAGGGCAACCCTGAGTGTGATGGGAAGACGGACTGTAGC 1844
Db 1745 CTCAATGGGCTCTGCTTGAGCAAGGGCAACCCTGAGTGTGACGGGAAGGAGGACTGTAGC 1804
Qy 1845 GATGGCTCCGATGAGAAAAACTGTGACTGTGGGCTGCGATCCTTTACCAAACAGGCTCGC 1904
Db 1805 GACGGCTCAGATGAGAAGGACTGCGACTGTGGGCTGCGGTCATTCACGAGACAGGCTCGT 1864
Qy 1905 GTGGTTGGTGGCACGAATGCGGACGAGGGCGAGTGGCCCTGGCAGGTGAGCCTCCACGCC 1964
Db 1865 GTTGTTGGGGGCACGGATGCGGATGAGGGCGAGTGGCCCTGGCAGGTAAGCCTGCATGCT 1924
Qy 1965 CTGGGCCAGGGCCACTTGTGTGGGGCCTCGCTCATCTCTCCTGACTGGCTGGTCTCTGCA 2024
Db 1925 CTGGGCCAGGGCCACATCTGCGGTGCTTCCCTCATCTCTCCCAACTGGCTGGTCTCTGCC 1984
Qy 2025 GCTCATTGCTTTCAGGATGACAAAAATTTCAAGTACTCAGACTACACGATGTGGACGGCC 2084
Db 1985 GCACACTGCTACATCGATGACAGAGGATTCAGGTACTCAGACCCCACGCAGTGGACGGCC 2044
Qy 2085 TTCCTGGGTCTGCTGGACCAGAGCAAGCGCAGTGCCTCTGGGGTGCAGGAGCTGAAGCTC 2144
Db 2045 TTCCTGGGCTTGCACGACCAGAGCCAGCGCAGCGCCCCTGGGGTGCAGGAGCGCAGGCTC 2104
Qy 2145 AAACGTATCATCACCCACCCTTCCTTCAATGATTTCACCTTCGACTATGACATCGCCTTG 2204
Db 2105 AAGCGCATCATCTCCCACCCCTTCTTCAATGACTTCACCTTCGACTATGACATCGCGCTG 2164
Qy 2205 CTGGAGCTGGAGAAGTCGGTGGAGTACAGCACCGTCGTGCGCCCCATCTGCCTGCCTGAT 2264
Db 2165 CTGGAGCTGGAGAAACCGGCAGAGTACAGCTCCATGGTGCGGCCCATCTGCCTGCCGGAC 2224
Qy 2265 GCTACCCATGTCTTCCCTGCTGGCAAGGCCATCTGGGTCACAGGCTGGGGGCACACAAAA 2324
Db 2225 GCCTCCCATGTCTTCCCTGCCGGCAAGGCCATCTGGGTCACGGGCTGGGGACACACCCAG 2284
Qy 2325 GAGGGAGGTACCGGAGCGCTGATCCTGCAGAAGGGTGAGATCCGTGTCATCAACCAGACC 2384
Db 2285 TATGGAGGCACTGGCGCGCTGATCCTGCAAAAGGGTGAGATCCGCGTCATCAACCAGACC 2344
Qy 2385 ACCTGTGAGGACCTCATGCCGCAGCAGATCACCCCACGAATGATGTGTGTGGGTTTCCTC 2444
Db 2345 ACCTGCGAGAACCTCCTGCCGCAGCAGATCACGCCGCGCATGATGTGCGTGGGCTTCCTC 2404

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Qy       2445 AGTGGGGGTGTGGACTCCTGCCAGGGTGACTCTGGTGGCCCCCTTGTCAAGCGCGGAGAAA 2504
Db       2405 AGCGGCGGCGTGGACTCCTGCCAGGGTGATTCCGGGGGACCCCTGTCCAGCGTGGAGGCG 2464

Qy       2505 GATGGGCGAATGTTCCAGGCTGGTGTGGTGAGCTGGGGTGAAGGCTGCGCTCAGAGGAAC 2564
Db       2465 GATGGGCGGATCTTCCAGGCCGGTGTGGTGAGCTGGGGAGACGGCTGCGCTCAGAGGAAC 2524

Qy       2565 AAGCCAGGCGTGTACACAAGGCTCCCTGTAGTTCGGGACTGGATCAAAGAGCACACTGGG 2624
Db       2525 AAGCCAGGCGTGTACACAAGGCTCCCTCTGTTTCGGGACTGGATCAAAGAGAACACTGGG 2584

Qy       2625 GTATAGCAGCATGGACAGACAGCCGACCACAAACACCCACAGGGATGCCCGACATGCACA 2684
Db       2585 GTATAGGGGCCGGG---GCCACCCAAATGTGTACACCTGCGGGGCCACCCATCGTCCACC 2641

Qy       2685 CCTGGATACAGGAGAGGAACACTGACGACATTTATGCTGTGGCCTCCCCCCCCCAACACA 2744
Db       2642 CCAGTGTGCACG-CCTGCAGGCTGGAGACTGGACCGCTGACTGCACCAGCGCCC-CCAGA 2699

Qy       2745 ACCCAGACTGTGAACTGCATCCTTAGGACTCAGAGT 2780
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; Sequence 3, Application US/10267219
; Publication No. US20030143219A1
; GENERAL INFORMATION:
;  APPLICANT: Madison, Edwin
;  APPLICANT:  Yeh, Jiunn-Chern
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING A TRANSMEMBRANE SERINE PROTEASE 2
;  TITLE OF INVENTION:  ENCODED POLYPEPTIDES AND METHODS BASED THEREON
;  FILE REFERENCE: 24745-1621
;  CURRENT APPLICATION NUMBER: US/10/267,219
;  CURRENT FILING DATE:  2002-10-08
;  PRIOR APPLICATION NUMBER: 60/328,530
;  PRIOR FILING DATE: 09-OCT-2001
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 3147
;   TYPE: DNA
;   ORGANISM: Homo Sapien
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1865)...(2590)
;   OTHER INFORMATION: Nucleic acid sequence of protease domain of MTSP1
US-10-267-219-3

  Query Match             60.6%;  Score 1883.2;  DB 13;  Length 3147;
  Best Local Similarity   81.2%;  Pred. No. 0;
  Matches 2223;  Conservative    0;  Mismatches  508;  Indels    5;  Gaps    3;

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Qy        105 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCTAGAGAACATGAATGGCTTTGAGGAG 164
Db         65 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCACGAGAAAGTGAATGGCTTGGAGGAA 124

Qy        165 GGTGTGGAGTTCCTGCCTGCGAACAATGCCAAGAAAGTGGAGAAGCGAGGCCCCAGGCGC 224
Db        125 GGCGTGGAGTTCCTGCCAGTCAACAACGTCAAGAAGGTGGAAAAGCATGGCCCGGGGCGC 184

Qy        225 TGGGTGGTGCTGGTGGCAGTGCTGTTCAGCTTCCTCTTGCTCTCCCTCATGGCTGGCTTG 284
Db        185 TGGGTGGTGCTGGCAGCCGTGCTGATCGGCCTCCTCTTGGTCTTGCTGGGGATCGGCTTC 244

Qy        285 CTGGTGTGGCACTTCCATTATCGGAATGTGCGGGTTCAAAAAGTCTTCAATGGCCATCTG 344
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Db        245 CTGGTGTGGCATTTGCAGTACCGGGACGTGCGTGTCCAGAAGGTCTTCAATGGCTACATG 304

Qy        345 AGGATCACAAATGAGATCTTTCTGGATGCGTATGAGAACTCCACCTCCACAGAGTTTATC 404
Db        305 AGGATCACAAATGAGAATTTTGTGGATGCCTACGAGAACTCCAACTCCACTGAGTTTGTA 364

Qy        405 AGCCTGGCCAGCCAGGTGAAGGAGGCGCTGAAGCTGCTGTACAATGAAGTCCCTGTCCTG 464
Db        365 AGCCTGGCCAGCAAGGTGAAGGACGCGCTGAAGCTGCTGTACAGCGGAGTCCCATTCCTG 424

Qy        465 GGTCCCTACCACAAGAAGTCGGCTGTAACTGCCTTCAGTGAGGGCAGTGTCATCGCCTAC 524
Db        425 GGCCCCTACCACAAGGAGTCGGCTGTGACGGCCTTCAGCGAGGGCAGCGTCATCGCCTAC 484

Qy        525 TACTGGTCAGAGTTCAGCATCCCCCCACACCTGGCAGAAGAGGTTGATCGCGCCATGGCT 584
Db        485 TACTGGTCTGAGTTCAGCATCCCGCAGCACCTGGTGGAGGAGGCCGAGCGCGTCATGGCC 544

Qy        585 GTGGAGCGAGTTGTAACATTGCCACCCCGAGCACGGGCACTGAAATCCTTCGTGCTAACA 644
Db        545 GAGGAGCGCGTAGTCATGCTGCCCCCGCGGGCGCGCTCCCTGAAGTCCTTTGTGGTCACC 604

Qy        645 TCTGTGGTGGCCTTCCCCATTGACCCCAGAATGCTGCAGAGGACTCAGGACAACAGCTGC 704
Db        605 TCAGTGGTGGCTTTCCCCACGGACTCCAAAACAGTACAGAGGACCCAGGACAACAGCTGC 664

Qy        705 AGTTTTGCCCTGCATGCCCATGGTGCAGCAGTGACACGCTTCACTACCCCTGGCTTCCCC 764
Db        665 AGCTTTGGCCTGCACGCCCGCGGTGTGGAGCTGATGCGCTTCACCACGCCCGGCTTCCCT 724

Qy        765 AACAGTCCCTACCCGGCGCATGCCCGCTGCCAGTGGGTCCTGCGGGGGGACGCCGACTCT 824
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Qy        825 GTGCTGAGCCTCACCTTCCGAAGCTTTGATGTCGCTCCCTGTGATGAGCATGGCAGTGAC 884
Db        785 GTGCTGAGCCTCACCTTCCGCAGCTTTGACCTTGCGTCCTGCGACGAGCGCGGCAGCGAC 844

Qy        885 CTGGTCACCGTGTATGATAGCCTGAGCCCCATGGAACCCCACGCTGTGGTGCGGCTGTGT 944
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Qy        945 GGCACCTTCTCACCCTCCTACAACCTGACTTTCCTCTCCTCCCAGAACGTCTTCCTTGTC 1004
Db        905 GGCACCTACCCTCCCTCCTACAACCTGACCTTCCACTCCTCCCAGAACGTCCTGCTCATC 964

Qy       1005 ACGCTGATAACCAATACTGACCGGCGACATCCTGGCTTTGAGGCCACTTTCTTCCAGCTG 1064
Db        965 ACACTGATAACCAACACTGAGCGGCGGCATCCCGGCTTTGAGGCCACCTTCTTCCAGCTG 1024

Qy       1065 CCCAAGATGAGCAGCTGTGGCGGCTTTTTGAGTGACACCCAAGGGACATTTAGCAGCCCC 1124
Db       1025 CCTAGGATGAGCAGCTGTGGAGGCCGCTTACGTAAAGCCCAGGGGACATTCAACAGCCCC 1084

Qy       1125 TACTATCCAGGCCACTACCCGCCCAACATCAACTGCACATGGAATATCAAGGTGCCCAAC 1184
Db       1085 TACTACCCAGGCCACTACCCACCCAACATTGACTGCACATGGAACATTGAGGTGCCCAAC 1144

Qy       1185 AACCGGAACGTGAAGGTGCGCTTCAAACTCTTCTATCTGGTGGACCCCAACGTACCAGTG 1244
Db       1145 AACCAGCATGTGAAGGTGAGCTTCAAATTCTTCTACCTGCTGGAGCCCGGCGTGCCTGCG 1204

Qy       1245 GGCTCCTGCACCAAGGACTATGTGGAGATCAACGGGGAGAAGTACTGCGGTGAGAGGTCC 1304
Db       1205 GGCACCTGCCCCAAGGACTACGTGGAGATCAATGGGGAGAAATACTGCGGAGAGAGGTCC 1264

Qy       1305 CAGTTTGTGGTGAGCAGCAACAGCAGCAAGATTACAGTCCACTTCCATTCTGATCACTCG 1364
Db       1265 CAGTTCGTCGTCACCAGCAACAGCAACAAGATCACAGTTCGCTTCCACTCAGATCAGTCC 1324

Qy       1365 TACACGGACACCGGGTTCCTAGCTGAGTACCTCTCCTACGACTCCAACGACCCGTGCCCA 1424
Db       1325 TACACCGACACCGGCTTCTTAGCTGAATACCTCTCCTACGACTCCAGTGACCCATGCCCG 1384
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Qy       1425 GGGATGTTCATGTGCAAGACTGGACGGTGCATCCGAAAGGAACTGCGCTGCGACGGCTGG 1484
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Qy       1485 GCAGACTGCCCGGATTATAGTGATGAGCGTTACTGCCGATGCAATGCCACCCACCAGTTC 1544
Db       1445 GCCGACTGCACCGACCACAGCGATGAGCTCAACTGCAGTTGCGACGCCGGCCACCAGTTC 1504

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Db       1505 ACGTGCAAGAACAAGTTCTGCAAGCCCCTCTTCTGGGTCTGCGACAGTGTGAACGACTGC 1564

Qy       1605 GGGGACGGAAGTGACGAGGAGGGCTGCAGCTGTCCTGCTGGGAGTTTCAAGTGTTCCAAT 1664
Db       1565 GGAGACAACAGCGACGAGCAGGGGTGCAGTTGTCCGGCCCAGACCTTCAGGTGTTCCAAT 1624

Qy       1665 GGGAAGTGTCTCCCTCAGAGCCAGAAGTGTAATGGGAAGGACAACTGTGGAGATGGGTCT 1724
Db       1625 GGGAAGTGCCTCTCGAAAAGCCAGCAGTGCAATGGGAAGGACGACTGTGGGGACGGGTCC 1684

Qy       1725 GACGAGGCTTCATGTGACAGCGTGAATGTCGTCTCTTGCACCAAATATACCTACCGCTGC 1784
Db       1685 GACGAGGCCTCCTGCCCCAAGGTGAACGTCGTCACTTGTACCAAACACACCTACCGCTGC 1744

Qy       1785 CAAAATGGCCTCTGTCTGAGCAAGGGCAACCCTGAGTGTGATGGGAAGACGGACTGTAGC 1844
Db       1745 CTCAATGGGCTCTGCTTGAGCAAGGGCAACCCTGAGTGTGACGGGAAGGAGGACTGTAGC 1804

Qy       1845 GATGGCTCCGATGAGAAAAACTGTGACTGTGGGCTGCGATCCTTTACCAAACAGGCTCGC 1904
Db       1805 GACGGCTCAGATGAGAAGGACTGCGACTGTGGGCTGCGGTCATTCACGAGACAGGCTCGT 1864

Qy       1905 GTGGTTGGTGGCACGAATGCGGACGAGGGCGAGTGGCCCTGGCAGGTGAGCCTCCACGCC 1964
Db       1865 GTTGTTGGGGGCACGGATGCGGATGAGGGCGAGTGGCCCTGGCAGGTAAGCCTGCATGCT 1924

Qy       1965 CTGGGCCAGGGCCACTTGTGTGGGGCCTCGCTCATCTCTCCTGACTGGCTGGTCTCTGCA 2024
Db       1925 CTGGGCCAGGGCCACATCTGCGGTGCTTCCCTCATCTCTCCCAACTGGCTGGTCTCTGCC 1984

Qy       2025 GCTCATTGCTTTCAGGATGACAAAAATTTCAAGTACTCAGACTACACGATGTGGACGGCC 2084
Db       1985 GCACACTGCTACATCGATGACAGAGGATTCAGGTACTCAGACCCCACGCAGTGGACGGCC 2044

Qy       2085 TTCCTGGGTCTGCTGGACCAGAGCAAGCGCAGTGCCTCTGGGGTGCAGGAGCTGAAGCTC 2144
Db       2045 TTCCTGGGCTTGCACGACCAGAGCCAGCGCAGCGCCCCTGGGGTGCAGGAGCGCAGGCTC 2104

Qy       2145 AAACGTATCATCACCCACCCTTCCTTCAATGATTTCACCTTCGACTATGACATCGCCTTG 2204
Db       2105 AAGCGCATCATCTCCCACCCCTTCTTCAATGACTTCACCTTCGACTATGACATCGCGCTG 2164

Qy       2205 CTGGAGCTGGAGAAGTCGGTGGAGTACAGCACCGTCGTGCGCCCCATCTGCCTGCCTGAT 2264
Db       2165 CTGGAGCTGGAGAAACCGGCAGAGTACAGCTCCATGGTGCGGCCCATCTGCCTGCCGGAC 2224

Qy       2265 GCTACCCATGTCTTCCCTGCTGGCAAGGCCATCTGGGTCACAGGCTGGGGGCACACAAAA 2324
Db       2225 GCCTCCCATGTCTTCCCTGCCGGCAAGGCCATCTGGGTCACGGGCTGGGGACACACCCAG 2284

Qy       2325 GAGGGAGGTACCGGAGCGCTGATCCTGCAGAAGGGTGAGATCCGTGTCATCAACCAGACC 2384
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Qy       2385 ACCTGTGAGGACCTCATGCCGCAGCAGATCACCCCACGAATGATGTGTGTGGGTTTCCTC 2444
Db       2345 ACCTGCGAGAACCTCCTGCCGCAGCAGATCACGCCGCGCATGATGTGCGTGGGCTTCCTC 2404

Qy       2445 AGTGGGGGTGTGGACTCCTGCCAGGGTGACTCTGGTGGCCCCTTGTCAAGCGCGGAGAAA 2504
Db       2405 AGCGGCGGCGTGGACTCCTGCCAGGGTGATTCCGGGGGACCCCTGTCCAGCGTGGAGGCG 2464
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Qy       2505 GATGGGCGAATGTTCCAGGCTGGTGTGGTGAGCTGGGGTGAAGGCTGCGCTCAGAGGAAC 2564
Db       2465 GATGGGCGGATCTTCCAGGCCGGTGTGGTGAGCTGGGGAGACGGCTGCGCTCAGAGGAAC 2524

Qy       2565 AAGCCAGGCGTGTACACAAGGCTCCCTGTAGTTCGGGACTGGATCAAAGAGCACACTGGG 2624
Db       2525 AAGCCAGGCGTGTACACAAGGCTCCCTCTGTTTCGGGACTGGATCAAAGAGAACACTGGG 2584

Qy       2625 GTATAGCAGCATGGACAGACAGCCGACCACAAACACCCACAGGGATGCCCGACATGCACA 2684
Db       2585 GTATAGGGGCCGGG---GCCACCCAAATGTGTACACCTGCGGGGCCACCCATCGTCCACC 2641

Qy       2685 CCTGGATACAGGAGAGGAACACTGACGACATTTATGCTGTGGCCTCCCCCCCCCAACACA 2744
Db       2642 CCAGTGTGCACG-CCTGCAGGCTGGAGACTGGACCGCTGACTGCACCAGCGCCC-CCAGA 2699

Qy       2745 ACCCAGACTGTGAACTGCATCCTTAGGACTCAGAGT 2780
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RESULT 12
US-10-302-840A-1
; Sequence 1, Application US/10302840A
; Publication No. US20030134794A1
; GENERAL INFORMATION:
; APPLICANT: Madison, Edwin L.
; APPLICANT: Ong, Edgar O.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING SERINE PROTEASE CVSP17, THE ENCODI
; TITLE OF INVENTION: POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: 24745-1622
; CURRENT APPLICATION NUMBER: US/10/302,840A
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/332,015
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3147
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (23)...(2589)
; OTHER INFORMATION: Nucleotide sequence encoding MTSP1
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank #AR081724
; DATABASE ENTRY DATE: 2000-08-31
US-10-302-840A-1

Query Match 60.6%; Score 1883.2; DB 13; Length 3147;
Best Local Similarity 81.2%; Pred. No. 0;
Matches 2223; Conservative 0; Mismatches 508; Indels 5; Gaps 3;

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Db          5 GAGCGGCCTCGGGGTACCATGGGGAGCGATCGGGCCCGCAAGGGCGGAGGGGGCCCGAAG 64

Qy        105 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCTAGAGAACATGAATGGCTTTGAGGAG 164
Db         65 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCACGAGAAAGTGAATGGCTTGGAGGAA 124

Qy        165 GGTGTGGAGTTCCTGCCTGCGAACAATGCCAAGAAAGTGGAGAAGCGAGGCCCCAGGCGC 224
Db        125 GGCGTGGAGTTCCTGCCAGTCAACAACGTCAAGAAGGTGGAAAAGCATGGCCCGGGGCGC 184

Qy        225 TGGGTGGTGCTGGTGGCAGTGCTGTTCAGCTTCCTCTTGCTCTCCCTCATGGCTGGCTTG 284
Db        185 TGGGTGGTGCTGGCAGCCGTGCTGATCGGCCTCCTCTTGGTCTTGCTGGGGATCGGCTTC 244

Qy        285 CTGGTGTGGCACTTCCATTATCGGAATGTGCGGGTTCAAAAAGTCTTCAATGGCCATCTG 344
Db        245 CTGGTGTGGCATTTGCAGTACCGGGACGTGCGTGTCCAGAAGGTCTTCAATGGCTACATG 304
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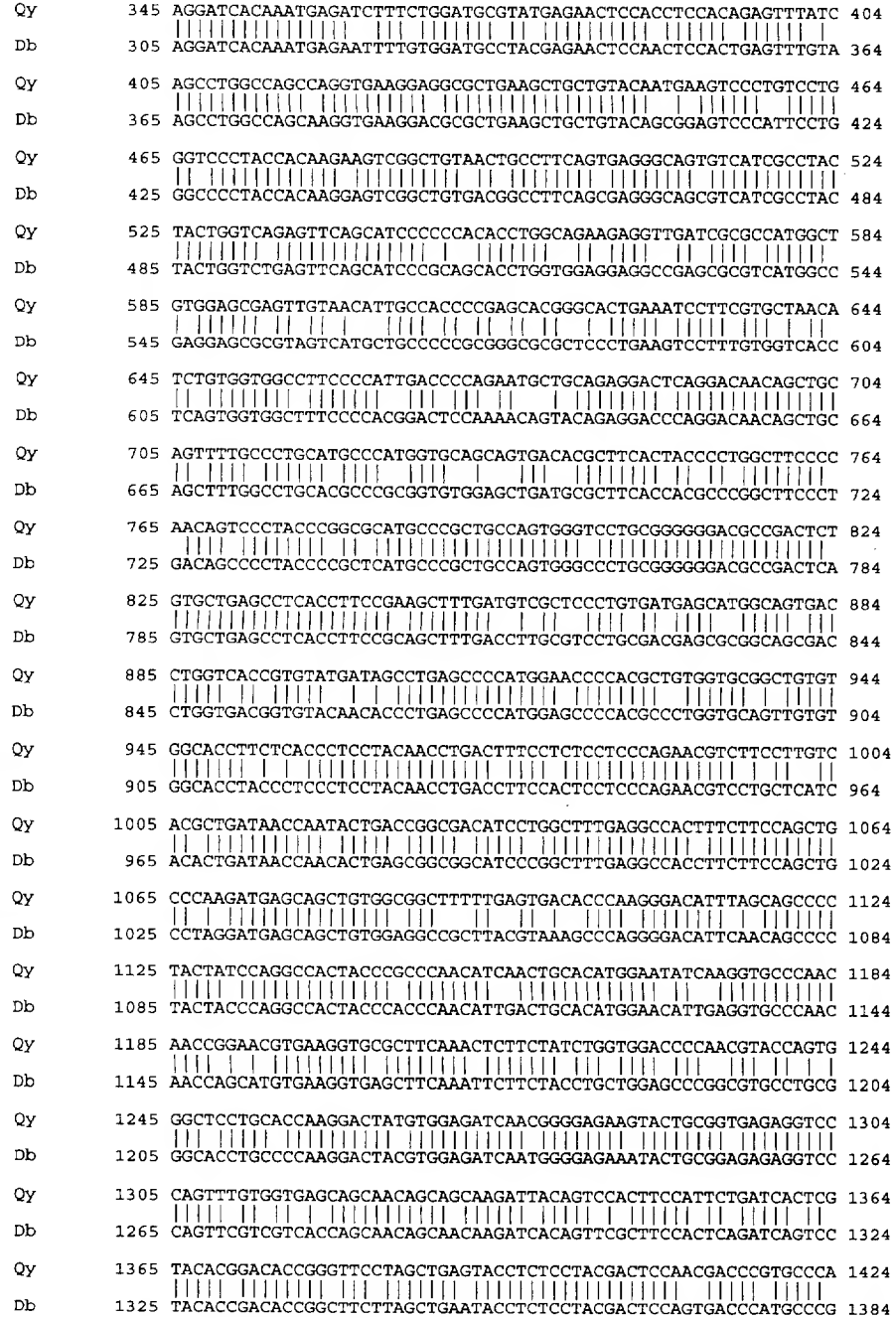
Qy 345 AGGATCACAAATGAGATCTTTCTGGATGCGTATGAGAACTCCACCTCCACAGAGTTTATC 404
Db 305 AGGATCACAAATGAGAATTTTGTGGATGCCTACGAGAACTCCAACTCCACTGAGTTTGTA 364
Qy 405 AGCCTGGCCAGCCAGGTGAAGGAGGCGCTGAAGCTGCTGTACAATGAAGTCCCTGTCCTG 464
Db 365 AGCCTGGCCAGCAAGGTGAAGGACGCGCTGAAGCTGCTGTACAGCGGAGTCCCATTCCTG 424
Qy 465 GGTCCCTACCACAAGAAGTCGGCTGTAACTGCCTTCAGTGAGGGCAGTGTCATCGCCTAC 524
Db 425 GGCCCCTACCACAAGGAGTCGGCTGTGACGGCCTTCAGCGAGGGCAGCGTCATCGCCTAC 484
Qy 525 TACTGGTCAGAGTTCAGCATCCCCCCACACCTGGCAGAAGAGGTTGATCGCGCCATGGCT 584
Db 485 TACTGGTCTGAGTTCAGCATCCCGCAGCACCTGGTGGAGGAGGCCGAGCGCGTCATGGCC 544
Qy 585 GTGGAGCGAGTTGTAACATTGCCACCCCGAGCACGGGCACTGAAATCCTTCGTGCTAACA 644
Db 545 GAGGAGCGCGTAGTCATGCTGCCCCCGCGGGCGCGCTCCCTGAAGTCCTTTGTGGTCACC 604
Qy 645 TCTGTGGTGGCCTTCCCCATTGACCCCAGAATGCTGCAGAGGACTCAGGACAACAGCTGC 704
Db 605 TCAGTGGTGGCTTTCCCCACGGACTCCAAAACAGTACAGAGGACCCAGGACAACAGCTGC 664
Qy 705 AGTTTTGCCCTGCATGCCCATGGTGCAGCAGTGACACGCTTCACTACCCCTGGCTTCCCC 764
Db 665 AGCTTTGGCCTGCACGCCCGCGGTGTGGAGCTGATGCGCTTCACCACGCCCGGCTTCCCT 724
Qy 765 AACAGTCCCTACCCGGCGCATGCCCGCTGCCAGTGGGTCCTGCGGGGGGACGCCGACTCT 824
Db 725 GACAGCCCCTACCCCGCTCATGCCCGCTGCCAGTGGGCCCTGCGGGGGGACGCCGACTCA 784
Qy 825 GTGCTGAGCCTCACCTTCCGAAGCTTTGATGTCGCTCCCTGTGATGAGCATGGCAGTGAC 884
Db 785 GTGCTGAGCCTCACCTTCCGCAGCTTTGACCTTGCGTCCTGCGACGAGCGCGGCAGCGAC 844
Qy 885 CTGGTCACCGTGTATGATAGCCTGAGCCCCATGGAACCCCACGCTGTGGTGCGGCTGTGT 944
Db 845 CTGGTGACGGTGTACAACACCCTGAGCCCCATGGAGCCCCACGCCCTGGTGCAGTTGTGT 904
Qy 945 GGCACCTTCTCACCCTCCTACAACCTGACTTTCCTCTCCTCCCAGAACGTCTTCCTTGTC 1004
Db 905 GGCACCTACCCTCCCTCCTACAACCTGACCTTCCACTCCTCCCAGAACGTCCTGCTCATC 964
Qy 1005 ACGCTGATAACCAATACTGACCGGCGACATCCTGGCTTTGAGGCCACTTTCTTCCAGCTG 1064
Db 965 ACACTGATAACCAACACTGAGCGGCGGCATCCCGGCTTTGAGGCCACCTTCTTCCAGCTG 1024
Qy 1065 CCCAAGATGAGCAGCTGTGGCGGCTTTTTGAGTGACACCCAAGGGACATTTAGCAGCCCC 1124
Db 1025 CCTAGGATGAGCAGCTGTGGAGGCCGCTTACGTAAAGCCCAGGGGACATTCAACAGCCCC 1084
Qy 1125 TACTATCCAGGCCACTACCCGCCCAACATCAACTGCACATGGAATATCAAGGTGCCCAAC 1184
Db 1085 TACTACCCAGGCCACTACCCACCCAACATTGACTGCACATGGAACATTGAGGTGCCCAAC 1144
Qy 1185 AACCGGAACGTGAAGGTGCGCTTCAAACTCTTCTATCTGGTGGACCCCAACGTACCAGTG 1244
Db 1145 AACCAGCATGTGAAGGTGAGCTTCAAATTCTTCTACCTGCTGGAGCCCGGCGTGCCTGCG 1204
Qy 1245 GGCTCCTGCACCAAGGACTATGTGGAGATCAACGGGGAGAAGTACTGCGGTGAGAGGTCC 1304
Db 1205 GGCACCTGCCCCAAGGACTACGTGGAGATCAATGGGGAGAAATACTGCGGAGAGAGGTCC 1264
Qy 1305 CAGTTTGTGGTGAGCAGCAACAGCAGCAAGATTACAGTCCACTTCCATTCTGATCACTCG 1364
Db 1265 CAGTTCGTCGTCACCAGCAACAGCAACAAGATCACAGTTCGCTTCCACTCAGATCAGTCC 1324
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Qy 1425 GGGATGTTCATGTGCAAGACTGGACGGTGCATCCGAAAGGAACTGCGCTGCGACGGCTGG 1484
Db 1385 GGGCAGTTCACGTGCCGCACGGGGCGGTGTATCCGGAAGGAGCTGCGCTGTGATGGCTGG 1444
Qy 1485 GCAGACTGCCCGGATTATAGTGATGAGCGTTACTGCCGATGCAATGCCACCCACCAGTTC 1544
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Qy 1545 ACGTGCAAAAACCAGTTCTGCAAGCCCCTCTTCTGGGTCTGTGACAGTGTCAACGACTGT 1604
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Qy 1605 GGGGACGGAAGTGACGAGGAGGGCTGCAGCTGTCCTGCTGGGAGTTTCAAGTGTTCCAAT 1664
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Qy 1665 GGGAAGTGTCTCCCTCAGAGCCAGAAGTGTAATGGGAAGGACAACTGTGGAGATGGGTCT 1724
Db 1625 GGGAAGTGCCTCTCGAAAAGCCAGCAGTGCAATGGGAAGGACGACTGTGGGGACGGGTCC 1684
Qy 1725 GACGAGGCTTCATGTGACAGCGTGAATGTCGTCTCTTGCACCAAATATACCTACCGCTGC 1784
Db 1685 GACGAGGCCTCCTGCCCCAAGGTGAACGTCGTCACTTGTACCAAACACACCTACCGCTGC 1744
Qy 1785 CAAAATGGCCTCTGTCTGAGCAAGGGCAACCCTGAGTGTGATGGGAAGACGGACTGTAGC 1844
Db 1745 CTCAATGGGCTCTGCTTGAGCAAGGGCAACCCTGAGTGTGACGGGAAGGAGGACTGTAGC 1804
Qy 1845 GATGGCTCCGATGAGAAAAACTGTGACTGTGGGCTGCGATCCTTTACCAAACAGGCTCGC 1904
Db 1805 GACGGCTCAGATGAGAAGGACTGCGACTGTGGGCTGCGGTCATTCACGAGACAGGCTCGT 1864
Qy 1905 GTGGTTGGTGGCACGAATGCGGACGAGGGCGAGTGGCCCTGGCAGGTGAGCCTCCACGCC 1964
Db 1865 GTTGTTGGGGGCACGGATGCGGATGAGGGCGAGTGGCCCTGGCAGGTAAGCCTGCATGCT 1924
Qy 1965 CTGGGCCAGGGCCACTTGTGTGGGGCCTCGCTCATCTCTCCTGACTGGCTGGTCTCTGCA 2024
Db 1925 CTGGGCCAGGGCCACATCTGCGGTGCTTCCCTCATCTCTCCCAACTGGCTGGTCTCTGCC 1984
Qy 2025 GCTCATTGCTTTCAGGATGACAAAAATTTCAAGTACTCAGACTACACGATGTGGACGGCC 2084
Db 1985 GCACACTGCTACATCGATGACAGAGGATTCAGGTACTCAGACCCCACGCAGTGGACGGCC 2044
Qy 2085 TTCCTGGGTCTGCTGGACCAGAGCAAGCGCAGTGCCTCTGGGGTGCAGGAGCTGAAGCTC 2144
Db 2045 TTCCTGGGCTTGCACGACCAGAGCCAGCGCAGCGCCCCTGGGGTGCAGGAGCGCAGGCTC 2104
Qy 2145 AAACGTATCATCACCCACCCTTCCTTCAATGATTTCACCTTCGACTATGACATCGCCTTG 2204
Db 2105 AAGCGCATCATCTCCCACCCCTTCTTCAATGACTTCACCTTCGACTATGACATCGCGCTG 2164
Qy 2205 CTGGAGCTGGAGAAGTCGGTGGAGTACAGCACCGTCGTGCGCCCCATCTGCCTGCCTGAT 2264
Db 2165 CTGGAGCTGGAGAAACCGGCAGAGTACAGCTCCATGGTGCGGCCCATCTGCCTGCCGGAC 2224
Qy 2265 GCTACCCATGTCTTCCCTGCTGGCAAGGCCATCTGGGTCACAGGCTGGGGGCACACAAAA 2324
Db 2225 GCCTCCCATGTCTTCCCTGCCGGCAAGGCCATCTGGGTCACGGGCTGGGGACACACCCAG 2284
Qy 2325 GAGGGAGGTACCGGAGCGCTGATCCTGCAGAAGGGTGAGATCCGTGTCATCAACCAGACC 2384
Db 2285 TATGGAGGCACTGGCGCGCTGATCCTGCAAAAGGGTGAGATCCGCGTCATCAACCAGACC 2344
Qy 2385 ACCTGTGAGGACCTCATGCCGCAGCAGATCACCCCACGAATGATGTGTGTGGGTTTCCTC 2444
Db 2345 ACCTGCGAGAACCTCCTGCCGCAGCAGATCACGCCGCGCATGATGTGCGTGGGCTTCCTC 2404
Qy 2445 AGTGGGGGTGTGGACTCCTGCCAGGGTGACTCTGGTGGCCCCCTTGTCAAGCGCGGAGAAA 2504
Db 2405 AGCGGCGGCGTGGACTCCTGCCAGGGTGATTCCGGGGGACCCCTGTCCAGCGTGGAGGCG 2464
Qy 2505 GATGGGCGAATGTTCCAGGCTGGTGTGGTGAGCTGGGGTGAAGGCTGCGCTCAGAGGAAC 2564

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Db       2465 GATGGGCGGATCTTCCAGGCCGGTGTGGTGAGCTGGGGAGACGGCTGCGCTCAGAGGAAC 2524

Qy       2565 AAGCCAGGCGTGTACACAAGGCTCCCTGTAGTTCGGGACTGGATCAAAGAGCACACTGGG 2624

Db       2525 AAGCCAGGCGTGTACACAAGGCTCCCTCTGTTTCGGGACTGGATCAAAGAGAACACTGGG 2584

Qy       2625 GTATAGCAGCATGGACAGACAGCCGACCACAAACACCCACAGGGATGCCCGACATGCACA 2684

Db       2585 GTATAGGGGCCGGG---GCCACCCAAATGTGTACACCTGCGGGGCCACCCATCGTCCACC 2641

Qy       2685 CCTGGATACAGGAGAGGAACACTGACGACATTTATGCTGTGGCCTCCCCCCCCCAACACA 2744

Db       2642 CCAGTGTGCACG-CCTGCAGGCTGGAGACTGGACCGCTGACTGCACCAGCGCCC-CCAGA 2699

Qy       2745 ACCCAGACTGTGAACTGCATCCTTAGGACTCAGAGT 2780

Db       2700 ACATACACTGTGAACTCAATCTCCAGGGCTCCAAAT 2735


RESULT 13
US-10-302-840A-3
; Sequence 3, Application US/10302840A
; Publication No. US20030134794A1
; GENERAL INFORMATION:
;  APPLICANT: Madison, Edwin L.
;  APPLICANT:  Ong, Edgar O.
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING SERINE PROTEASE CVSP17, THE ENCOD
;  TITLE OF INVENTION:  POLYPEPTIDES AND METHODS BASED THEREON
;  FILE REFERENCE: 24745-1622
;  CURRENT APPLICATION NUMBER: US/10/302,840A
;  CURRENT FILING DATE:  2003-01-24
;  PRIOR APPLICATION NUMBER: 60/332,015
;  PRIOR FILING DATE: 2001-11-20
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 3147
;   TYPE: DNA
;   ORGANISM: Homo Sapien
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1865)...(2590)
;   OTHER INFORMATION: Nucleic acid sequence of protease domain of MTSP1
US-10-302-840A-3

  Query Match           60.6%;  Score 1883.2;  DB 13;  Length 3147;
  Best Local Similarity  81.2%;  Pred. No. 0;
  Matches 2223;  Conservative    0;  Mismatches  508;  Indels    5;  Gaps    3;

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Db         65 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCACGAGAAAGTGAATGGCTTGGAGGAA 124

Qy        165 GGTGTGGAGTTCCTGCCTGCGAACAATGCCAAGAAAGTGGAGAAGCGAGGCCCCAGGCGC 224

Db        125 GGCGTGGAGTTCCTGCCAGTCAACAACGTCAAGAAGGTGGAAAAGCATGGCCCGGGGCGC 184

Qy        225 TGGGTGGTGCTGGTGGCAGTGCTGTTCAGCTTCCTCTTGCTCTCCCTCATGGCTGGCTTG 284

Db        185 TGGGTGGTGCTGGCAGCCGTGCTGATCGGCCTCCTCTTGGTCTTGCTGGGGATCGGCTTC 244

Qy        285 CTGGTGTGGCACTTCCATTATCGGAATGTGCGGGTTCAAAAAGTCTTCAATGGCCATCTG 344

Db        245 CTGGTGTGGCATTTGCAGTACCGGGACGTGCGTGTCCAGAAGGTCTTCAATGGCTACATG 304

Qy        345 AGGATCACAAATGAGATCTTTCTGGATGCGTATGAGAACTCCACCTCCACAGAGTTTATC 404

Db        305 AGGATCACAAATGAGAATTTTGTGGATGCCTACGAGAACTCCAACTCCACTGAGTTTGTA 364

Qy        405 AGCCTGGCCAGCCAGGTGAAGGAGGCGCTGAAGCTGCTGTACAATGAAGTCCCTGTCCTG 464

Db        365 AGCCTGGCCAGCAAGGTGAAGGACGCGCTGAAGCTGCTGTACAGCGGAGTCCCATTCCTG 424

Qy        465 GGTCCCTACCACAAGAAGTCGGCTGTAACTGCCTTCAGTGAGGGCAGTGTCATCGCCTAC 524

Db        425 GGCCCCTACCACAAGGAGTCGGCTGTGACGGCCTTCAGCGAGGGCAGCGTCATCGCCTAC 484

Qy        525 TACTGGTCAGAGTTCAGCATCCCCCCACACCTGGCAGAAGAGGTTGATCGCGCCATGGCT 584

Db        485 TACTGGTCTGAGTTCAGCATCCCGCAGCACCTGGTGGAGGAGGCCGAGCGCGTCATGGCC 544

Qy        585 GTGGAGCGAGTTGTAACATTGCCACCCCGAGCACGGGCACTGAAATCCTTCGTGCTAACA 644

Db        545 GAGGAGCGCGTAGTCATGCTGCCCCCGCGGGCGCGCTCCCTGAAGTCCTTTGTGGTCACC 604

Qy        645 TCTGTGGTGGCCTTCCCCATTGACCCCAGAATGCTGCAGAGGACTCAGGACAACAGCTGC 704

Db        605 TCAGTGGTGGCTTTCCCCACGGACTCCAAAACAGTACAGAGGACCCAGGACAACAGCTGC 664

Qy        705 AGTTTTGCCCTGCATGCCCATGGTGCAGCAGTGACACGCTTCACTACCCCTGGCTTCCCC 764

Db        665 AGCTTTGGCCTGCACGCCCGCGGTGTGGAGCTGATGCGCTTCACCACGCCCGGCTTCCCT 724

Qy        765 AACAGTCCCTACCCGGCGCATGCCCGCTGCCAGTGGGTCCTGCGGGGGGACGCCGACTCT 824

Db        725 GACAGCCCCTACCCCGCTCATGCCCGCTGCCAGTGGGCCCTGCGGGGGGACGCCGACTCA 784

Qy        825 GTGCTGAGCCTCACCTTCCGAAGCTTTGATGTCGCTCCCTGTGATGAGCATGGCAGTGAC 884

Db        785 GTGCTGAGCCTCACCTTCCGCAGCTTTGACCTTGCGTCCTGCGACGAGCGCGGCAGCGAC 844

Qy        885 CTGGTCACCGTGTATGATAGCCTGAGCCCCATGGAACCCCACGCTGTGGTGCGGCTGTGT 944

Db        845 CTGGTGACGGTGTACAACACCCTGAGCCCCATGGAGCCCCACGCCCTGGTGCAGTTGTGT 904

Qy        945 GGCACCTTCTCACCCTCCTACAACCTGACTTTCCTCTCCTCCCAGAACGTCTTCCTTGTC 1004

Db        905 GGCACCTACCCTCCCTCCTACAACCTGACCTTCCACTCCTCCCAGAACGTCCTGCTCATC 964

Qy       1005 ACGCTGATAACCAATACTGACCGGCGACATCCTGGCTTTGAGGCCACTTTCTTCCAGCTG 1064

Db        965 ACACTGATAACCAACACTGAGCGGCGGCATCCCGGCTTTGAGGCCACCTTCTTCCAGCTG 1024

Qy       1065 CCCAAGATGAGCAGCTGTGGCGGCTTTTTGAGTGACACCCAAGGGACATTTAGCAGCCCC 1124

Db       1025 CCTAGGATGAGCAGCTGTGGAGGCCGCTTACGTAAAGCCCAGGGGACATTCAACAGCCCC 1084

Qy       1125 TACTATCCAGGCCACTACCCGCCCAACATCAACTGCACATGGAATATCAAGGTGCCCAAC 1184

Db       1085 TACTACCCAGGCCACTACCCACCCAACATTGACTGCACATGGAACATTGAGGTGCCCAAC 1144

Qy       1185 AACCGGAACGTGAAGGTGCGCTTCAAACTCTTCTATCTGGTGGACCCCAACGTACCAGTG 1244

Db       1145 AACCAGCATGTGAAGGTGAGCTTCAAATTCTTCTACCTGCTGGAGCCCGGCGTGCCTGCG 1204

Qy       1245 GGCTCCTGCACCAAGGACTATGTGGAGATCAACGGGGAGAAGTACTGCGGTGAGAGGTCC 1304

Db       1205 GGCACCTGCCCCAAGGACTACGTGGAGATCAATGGGGAGAAATACTGCGGAGAGAGGTCC 1264

Qy       1305 CAGTTTGTGGTGAGCAGCAACAGCAGCAAGATTACAGTCCACTTCCATTCTGATCACTCG 1364

Db       1265 CAGTTCGTCGTCACCAGCAACAGCAACAAGATCACAGTTCGCTTCCACTCAGATCAGTCC 1324

Qy       1365 TACACGGACACCGGGTTCCTAGCTGAGTACCTCTCCTACGACTCCAACGACCCGTGCCCA 1424

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Qy       1425 GGGATGTTCATGTGCAAGACTGGACGGTGCATCCGAAAGGAACTGCGCTGCGACGGCTGG 1484

Db       1385 GGGCAGTTCACGTGCCGCACGGGGCGGTGTATCCGGAAGGAGCTGCGCTGTGATGGCTGG 1444
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Qy       1485 GCAGACTGCCCGGATTATAGTGATGAGCGTTACTGCCGATGCAATGCCACCCACCAGTTC 1544
Db       1445 GCCGACTGCACCGACCACAGCGATGAGCTCAACTGCAGTTGCGACGCCGGCCACCAGTTC 1504

Qy       1545 ACGTGCAAAAACCAGTTCTGCAAGCCCCTCTTCTGGGTCTGTGACAGTGTCAACGACTGT 1604
Db       1505 ACGTGCAAGAACAAGTTCTGCAAGCCCCTCTTCTGGGTCTGCGACAGTGTGAACGACTGC 1564

Qy       1605 GGGGACGGAAGTGACGAGGAGGGCTGCAGCTGTCCTGCTGGGAGTTTCAAGTGTTCCAAT 1664
Db       1565 GGAGACAACAGCGACGAGCAGGGGTGCAGTTGTCCGGCCCAGACCTTCAGGTGTTCCAAT 1624

Qy       1665 GGGAAGTGTCTCCCTCAGAGCCAGAAGTGTAATGGGAAGGACAACTGTGGAGATGGGTCT 1724
Db       1625 GGGAAGTGCCTCTCGAAAAGCCAGCAGTGCAATGGGAAGGACGACTGTGGGGACGGGTCC 1684

Qy       1725 GACGAGGCTTCATGTGACAGCGTGAATGTCGTCTCTTGCACCAAATATACCTACCGCTGC 1784
Db       1685 GACGAGGCCTCCTGCCCCAAGGTGAACGTCGTCACTTGTACCAAACACACCTACCGCTGC 1744

Qy       1785 CAAAATGGCCTCTGTCTGAGCAAGGGCAACCCTGAGTGTGATGGGAAGACGGACTGTAGC 1844
Db       1745 CTCAATGGGCTCTGCTTGAGCAAGGGCAACCCTGAGTGTGACGGGAAGGAGGACTGTAGC 1804

Qy       1845 GATGGCTCCGATGAGAAAAACTGTGACTGTGGGCTGCGATCCTTTACCAAACAGGCTCGC 1904
Db       1805 GACGGCTCAGATGAGAAGGACTGCGACTGTGGGCTGCGGTCATTCACGAGACAGGCTCGT 1864

Qy       1905 GTGGTTGGTGGCACGAATGCGGACGAGGGCGAGTGGCCCTGGCAGGTGAGCCTCCACGCC 1964
Db       1865 GTTGTTGGGGGCACGGATGCGGATGAGGGCGAGTGGCCCTGGCAGGTAAGCCTGCATGCT 1924

Qy       1965 CTGGGCCAGGGCCACTTGTGTGGGGCCTCGCTCATCTCTCCTGACTGGCTGGTCTCTGCA 2024
Db       1925 CTGGGCCAGGGCCACATCTGCGGTGCTTCCCTCATCTCTCCCAACTGGCTGGTCTCTGCC 1984

Qy       2025 GCTCATTGCTTTCAGGATGACAAAAATTTCAAGTACTCAGACTACACGATGTGGACGGCC 2084
Db       1985 GCACACTGCTACATCGATGACAGAGGATTCAGGTACTCAGACCCCACGCAGTGGACGGCC 2044

Qy       2085 TTCCTGGGTCTGCTGGACCAGAGCAAGCGCAGTGCCTCTGGGGTGCAGGAGCTGAAGCTC 2144
Db       2045 TTCCTGGGCTTGCACGACCAGAGCCAGCGCAGCGCCCCTGGGGTGCAGGAGCGCAGGCTC 2104

Qy       2145 AAACGTATCATCACCCACCCTTCCTTCAATGATTTCACCTTCGACTATGACATCGCCTTG 2204
Db       2105 AAGCGCATCATCTCCCACCCCTTCTTCAATGACTTCACCTTCGACTATGACATCGCGCTG 2164

Qy       2205 CTGGAGCTGGAGAAGTCGGTGGAGTACAGCACCGTCGTGCGCCCCATCTGCCTGCCTGAT 2264
Db       2165 CTGGAGCTGGAGAAACCGGCAGAGTACAGCTCCATGGTGCGGCCCATCTGCCTGCCGGAC 2224

Qy       2265 GCTACCCATGTCTTCCCTGCTGGCAAGGCCATCTGGGTCACAGGCTGGGGGCACACAAAA 2324
Db       2225 GCCTCCCATGTCTTCCCTGCCGGCAAGGCCATCTGGGTCACGGGCTGGGGACACACCCAG 2284

Qy       2325 GAGGGAGGTACCGGAGCGCTGATCCTGCAGAAGGGTGAGATCCGTGTCATCAACCAGACC 2384
Db       2285 TATGGAGGCACTGGCGCGCTGATCCTGCAAAAGGGTGAGATCCGCGTCATCAACCAGACC 2344

Qy       2385 ACCTGTGAGGACCTCATGCCGCAGCAGATCACCCCACGAATGATGTGTGTGGGTTTCCTC 2444
Db       2345 ACCTGCGAGAACCTCCTGCCGCAGCAGATCACGCCGCGCATGATGTGCGTGGGCTTCCTC 2404

Qy       2445 AGTGGGGGTGTGGACTCCTGCCAGGGTGACTCTGGTGGCCCCTTGTCAAGCGCGGAGAAA 2504
Db       2405 AGCGGCGGCGTGGACTCCTGCCAGGGTGATTCCGGGGGACCCCTGTCCAGCGTGGAGGCG 2464

Qy       2505 GATGGGCGAATGTTCCAGGCTGGTGTGGTGAGCTGGGGTGAAGGCTGCGCTCAGAGGAAC 2564
Db       2465 GATGGGCGGATCTTCCAGGCCGGTGTGGTGAGCTGGGGAGACGGCTGCGCTCAGAGGAAC 2524

Qy       2565 AAGCCAGGCGTGTACACAAGGCTCCCTGTAGTTCGGGACTGGATCAAAGAGCACACTGGG 2624
Db       2525 AAGCCAGGCGTGTACACAAGGCTCCCTCTGTTTCGGGACTGGATCAAAGAGAACACTGGG 2584

Qy       2625 GTATAGCAGCATGGACAGACAGCCGACCACAAACACCCACAGGGATGCCCGACATGCACA 2684
Db       2585 GTATAGGGGCCGGG---GCCACCCAAATGTGTACACCTGCGGGGCCACCCATCGTCCACC 2641

Qy       2685 CCTGGATACAGGAGAGGAACACTGACGACATTTATGCTGTGGCCTCCCCCCCCCAACACA 2744
Db       2642 CCAGTGTGCACG-CCTGCAGGCTGGAGACTGGACCGCTGACTGCACCAGCGCCC-CCAGA 2699

Qy       2745 ACCCAGACTGTGAACTGCATCCTTAGGACTCAGAGT 2780
Db       2700 ACATACACTGTGAACTCAATCTCCAGGGCTCCAAAT 2735
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RESULT 14
US-10-112-221A-1
; Sequence 1, Application US/10112221A
; Publication No. US20030166851A1
; GENERAL INFORMATION:
; APPLICANT: Madison, Edwin
; APPLICANT: Ong, Edgar O.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING A TRANSMEMBRANE SERINE PROTEASE 9,
; TITLE OF INVENTION: ENCODED POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: 24745-1615
; CURRENT APPLICATION NUMBER: US/10/112,221A
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 60/279,228
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 60/291,501
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3147
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (23)...(2589)
; OTHER INFORMATION: Nucleotide sequence encoding MTSP1
; PUBLICATION INFORMATION:
; AUTHORS: O'Brien, T.J. and Tanimoto, H.
; DATABASE ACCESSION NUMBER: GenBank #AR081724
; DATABASE ENTRY DATE: 2000-08-31
; PATENT DOCUMENT NUMBER: 5,972,616
; PATENT FILING DATE: 1998-02-20
; PUBLICATION DATE: 1999-10-26
US-10-112-221A-1

Query Match 60.6%; Score 1883.2; DB 13; Length 3147;
Best Local Similarity 81.2%; Pred. No. 0;
Matches 2223; Conservative 0; Mismatches 508; Indels 5; Gaps 3;

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Qy         45 GATCGGACCGCCAAAACCATGGGTAGCAATCGGGGCCGCAAGGCCGGAGGGGGCTCTCAG 104
Db          5 GAGCGGCCTCGGGGTACCATGGGGAGCGATCGGGCCCGCAAGGGCGGAGGGGGCCCGAAG 64

Qy        105 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCTAGAGAACATGAATGGCTTTGAGGAG 164
Db         65 GACTTCGGCGCGGGACTCAAGTACAACTCCCGGCACGAGAAAGTGAATGGCTTGGAGGAA 124

Qy        165 GGTGTGGAGTTCCTGCCTGCGAACAATGCCAAGAAAGTGGAGAAGCGAGGCCCCAGGCGC 224
Db        125 GGCGTGGAGTTCCTGCCAGTCAACAACGTCAAGAAGGTGGAAAAGCATGGCCCGGGGCGC 184

Qy        225 TGGGTGGTGCTGGTGGCAGTGCTGTTCAGCTTCCTCTTGCTCTCCCTCATGGCTGGCTTG 284
Db        185 TGGGTGGTGCTGGCAGCCGTGCTGATCGGCCTCCTCTTGGTCTTGCTGGGGATCGGCTTC 244

Qy        285 CTGGTGTGGCACTTCCATTATCGGAATGTGCGGGTTCAAAAAGTCTTCAATGGCCATCTG 344
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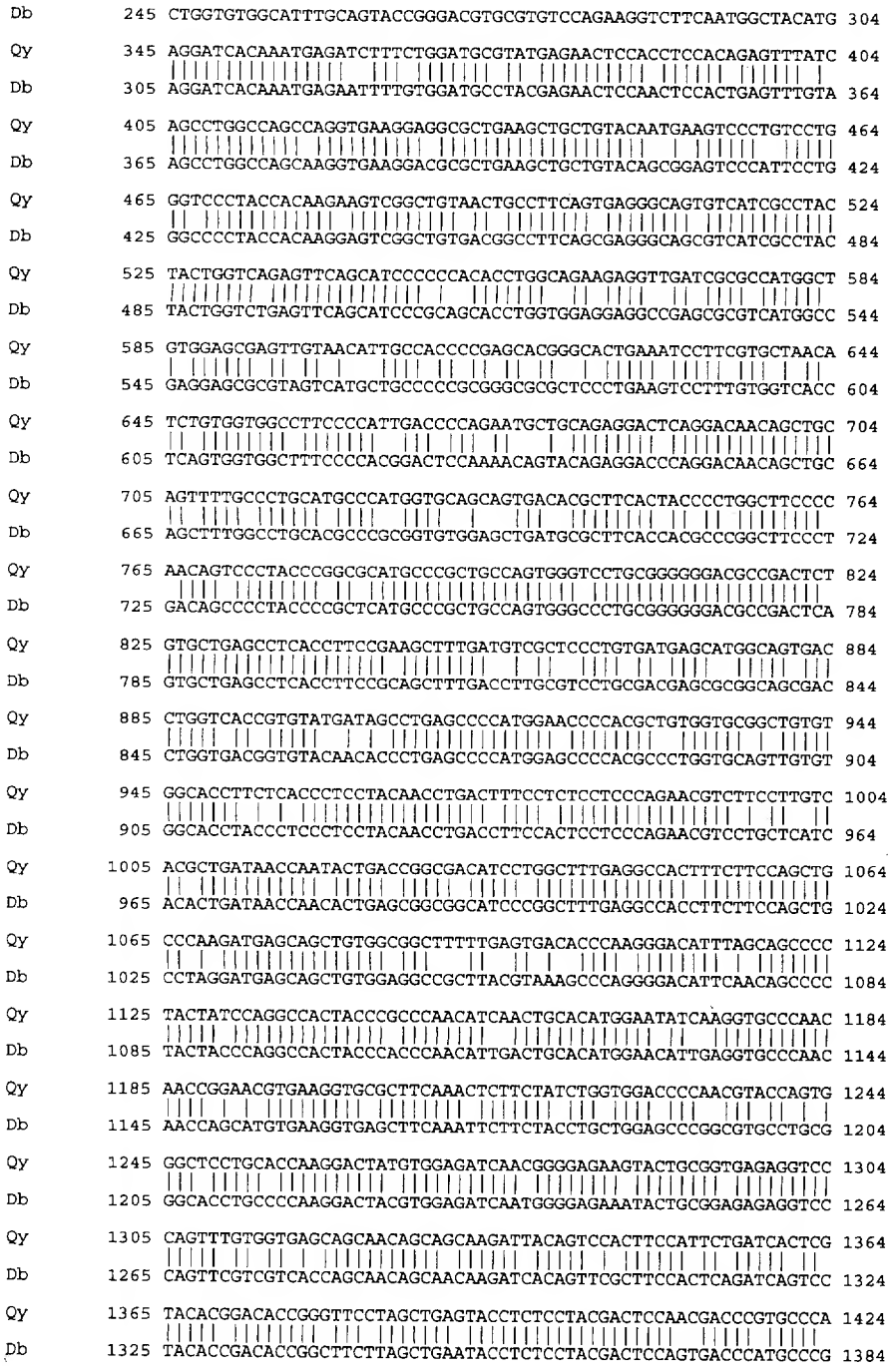

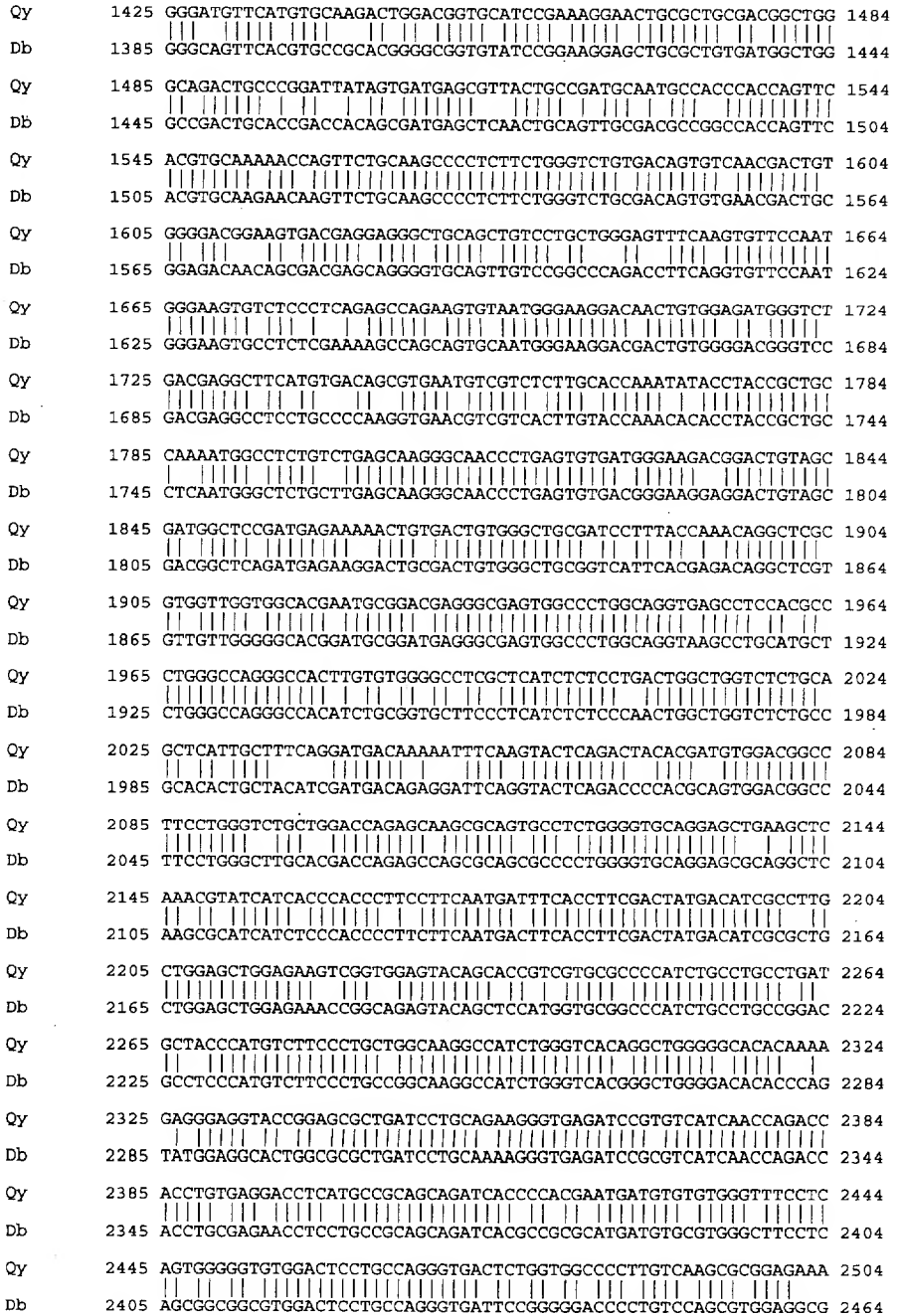

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Qy       2505 GATGGGCGAATGTTCCAGGCTGGTGTGGTGAGCTGGGGTGAAGGCTGCGCTCAGAGGAAC 2564
Db       2465 GATGGGCGGATCTTCCAGGCCGGTGTGGTGAGCTGGGGAGACGGCTGCGCTCAGAGGAAC 2524

Qy       2565 AAGCCAGGCGTGTACACAAGGCTCCCTGTAGTTCGGGACTGGATCAAAGAGCACACTGGG 2624
Db       2525 AAGCCAGGCGTGTACACAAGGCTCCCTCTGTTTCGGGACTGGATCAAAGAGAACACTGGG 2584

Qy       2625 GTATAGCAGCATGGACAGACAGCCGACCACAAACACCCACAGGGATGCCCGACATGCACA 2684
Db       2585 GTATAGGGGCCGGG---GCCACCCAAATGTGTACACCTGCGGGGCCACCCATCGTCCACC 2641

Qy       2685 CCTGGATACAGGAGAGGAACACTGACGACATTTATGCTGTGGCCTCCCCCCCCCCAACACA 2744
Db       2642 CCAGTGTGCACG-CCTGCAGGCTGGAGACTGGACCGCTGACTGCACCAGCGCCC-CCAGA 2699

Qy       2745 ACCCAGACTGTGAACTGCATCCTTAGGACTCAGAGT 2780
Db       2700 ACATACACTGTGAACTCAATCTCCAGGGCTCCAAAT 2735


RESULT 15
US-10-112-221A-3
; Sequence 3, Application US/10112221A
; Publication No. US20030166851A1
; GENERAL INFORMATION:
;  APPLICANT: Madison, Edwin
;  APPLICANT:  Ong, Edgar O.
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING A TRANSMEMBRANE SERINE PROTEASE 9
;  TITLE OF INVENTION:  ENCODED POLYPEPTIDES AND METHODS BASED THEREON
;  FILE REFERENCE: 24745-1615
;  CURRENT APPLICATION NUMBER: US/10/112,221A
;  CURRENT FILING DATE:  2002-03-27
;  PRIOR APPLICATION NUMBER: 60/279,228
;  PRIOR FILING DATE: 2001-03-27
;  PRIOR APPLICATION NUMBER: 60/291,501
;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 3147
;   TYPE: DNA
;   ORGANISM: Homo Sapien
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1865)...(2590)
;   OTHER INFORMATION: Nucleic acid sequence of protease domain of MTSP1
US-10-112-221A-3

  Query Match             60.6%;  Score 1883.2;  DB 13;  Length 3147;
  Best Local Similarity   81.2%;  Pred. No. 0;
  Matches 2223;  Conservative    0;  Mismatches  508;  Indels    5;  Gaps    3;

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Qy        525 TACTGGTCAGAGTTCAGCATCCCCCCACACCTGGCAGAAGAGGTTGATCGCGCCATGGCT 584
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Db       2045 TTCCTGGGCTTGCACGACCAGAGCCAGCGCAGCGCCCCTGGGGTGCAGGAGCGCAGGCTC 2104

Qy       2145 AAACGTATCATCACCCACCCTTCCTTCAATGATTTCACCTTCGACTATGACATCGCCTTG 2204

Db       2105 AAGCGCATCATCTCCCACCCCTTCTTCAATGACTTCACCTTCGACTATGACATCGCGCTG 2164

Qy       2205 CTGGAGCTGGAGAAGTCGGTGGAGTACAGCACCGTCGTGCGCCCCCATCTGCCTGCCTGAT 2264

Db       2165 CTGGAGCTGGAGAAACCGGCAGAGTACAGCTCCATGGTGCGGCCCATCTGCCTGCCGGAC 2224

Qy       2265 GCTACCCATGTCTTCCCTGCTGGCAAGGCCATCTGGGTCACAGGCTGGGGGCACACAAAA 2324

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Job time : 1070 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 21, 2004, 02:06:37 ; Search time 6211 Seconds
(without alignments)
12154.195 Million cell updates/sec

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Perfect score: 3106
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: em_estba:*
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27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3102.8	99.9	3248	11	BC008514	BC008514 Mus muscu
2	3087.6	99.4	4017	11	AK052738	AK052738 Mus muscu
3	956.4	30.8	2689	11	AK085410	AK085410 Mus muscu
4	843.8	27.2	944	13	BQ885551	BQ885551 AGENCOURT
5	833.6	26.8	884	12	BI688367	BI688367 603316692
6	788.8	25.4	803	12	BI690615	BI690615 603314210
7	778.2	25.1	990	13	BQ951529	BQ951529 AGENCOURT
8	760.4	24.5	762	12	BG919617	BG919617 602823173
9	759.4	24.4	874	14	CB208872	CB208872 AGENCOURT
10	747.2	24.1	798	12	BI664081	BI664081 603289385
11	739.2	23.8	746	14	BY756896	BY756896 BY756896
12	739.2	23.8	846	12	BI416218	BI416218 602989878
13	735.8	23.7	1116	10	BF301347	BF301347 602029796
14	732	23.6	786	12	BI646380	BI646380 603276244
15	721	23.2	928	12	BG915045	BG915045 602814325
16	720.8	23.2	777	12	BI150180	BI150180 602848502
17	716	23.1	928	12	BI694441	BI694441 603348025
18	710.8	22.9	838	12	BI656113	BI656113 603284774
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20	706.8	22.8	840	12	BI453178	BI453178 603173173
21	706.2	22.7	939	14	CA976536	CA976536 AGENCOURT
22	692.6	22.3	725	12	BI248406	BI248406 602967029
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25	684.4	22.0	697	12	BI853355	BI853355 603379936
26	681.8	22.0	708	12	BI078327	BI078327 602872681
27	681.2	21.9	838	13	BU152438	BU152438 AGENCOURT
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38	623.4	20.1	854	12	BI416184	BI416184 602989813
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ALIGNMENTS

RESULT 1
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DEFINITION Mus musculus, suppression of tumorigenicity 14 (colon carcinoma), clone IMAGE:3489914, mRNA.
ACCESSION BC008514
VERSION BC008514.1 GI:14250187
KEYWORDS HTC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 3248)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (25-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 7 Row: h Column: 16
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6677898
This clone has the following problem: no 5' EST match.

FEATURES Location/Qualifiers
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/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3489914"
/tissue_type="Mammary tumor. WAP-TGF alpha model. 7 months old, gross tissue."
/clone_lib="NCI_CGAP_Mam5"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

BASE COUNT 734 a 918 c 928 g 668 t
ORIGIN

Query Match 99.9%; Score 3102.8; DB 11; Length 3248;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3104; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy         61 CCATGGGTAGCAATCGGGGCCGCAAGGCCGGAGGGGGCTCTCAGGACTTCGGCGCGGGAC 120
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RESULT 2
AK052738
LOCUS AK052738 4017 bp mRNA linear HTC 05-DEC-2002
DEFINITION Mus musculus 0 day neonate kidney cDNA, RIKEN full-length enriched library, clone:D630041B06 product:suppression of tumorigenicity 14 (colon carcinoma), full insert sequence.
ACCESSION AK052738
VERSION AK052738.1 GI:26342936
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,

Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851

REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 4017)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers
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BASE COUNT 861 a 1098 c 1164 g 894 t
ORIGIN

Query Match 99.4%; Score 3087.6; DB 11; Length 4017;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3090; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy     1741 ACAGCGTGAATGTCGTCTCTTGCACCAAATATACCTACCGCTGCCAAAATGGCCTCTGTC 1800
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Db     1852 ACAGCGTGAATGTCGTCTCTTGCACCAAATATACCTACCGCTGCCAAAATGGCCTCTGTC 1911

Qy     1801 TGAGCAAGGGCAACCCTGAGTGTGATGGGAAGACGGACTGTAGCGATGGCTCCGATGAGA 1860
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Db     1912 TGAGCAAGGGCAACCCTGAGTGTGATGGGAAGACGGACTGTAGCGATGGCTCCGATGAGA 1971

Qy     1861 AAAACTGTGACTGTGGGCTGCGATCCTTTACCAAACAGGCTCGCGTGGTTGGTGGCACGA 1920
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Db     1972 AAAACTGTGACTGTGGGCTGCGATCCTTTACCAAACAGGCTCGCGTGGTTGGTGGCACGA 2031

Qy     1921 ATGCGGACGAGGGCGAGTGGCCCTGGCAGGTGAGCCTCCACGCCCTGGGCCAGGGCCACT 1980
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Qy     1981 TGTGTGGGGCCTCGCTCATCTCTCCTGACTGGCTGGTCTCTGCAGCTCATTGCTTTCAGG 2040
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Qy     2041 ATGACAAAAATTTCAAGTACTCAGACTACACGATGTGGACGGCCTTCCTGGGTCTGCTGG 2100
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Qy     2161 ACCCTTCCTTCAATGATTTCACCTTCGACTATGACATCGCCTTGCTGGAGCTGGAGAAGT 2220
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Db     2272 ACCCTTCCTTCAATGATTTCACCTTCGACTATGACATCGCCTTGCTGGAGCTGGAGAAGT 2331

Qy     2221 CGGTGGAGTACAGCACCGTCGTGCGCCCCATCTGCCTGCCTGATGCTACCCATGTCTTCC 2280
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Qy     2281 CTGCTGGCAAGGCCATCTGGGTCACAGGCTGGGGGCACACAAAAGAGGGAGGTACCGGAG 2340
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Qy     2581 CAAGGCTCCCTGTAGTTCGGGACTGGATCAAAGAGCACACTGGGGTATAGCAGCATGGAC 2640
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Db       3172 TTGAGAGTAAAACATTTTATTTCTTTTTAGGTAA 3205

RESULT 3
AK085410
LOCUS       AK085410               2689 bp    mRNA    linear   HTC 05-DEC-2002
DEFINITION  Mus musculus 0 day neonate kidney cDNA, RIKEN full-length enriched
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            (colon carcinoma), full insert sequence.
ACCESSION   AK085410
VERSION     AK085410.1  GI:26102691
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
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            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
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            Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
            Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
  MEDLINE   21085660
   PUBMED   11217851
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 2689)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
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            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.go.jp/
            URL:http://fantom.gsc.riken.go.jp/.
FEATURES             Location/Qualifiers
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ORIGIN

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  Matches 1415;  Conservative    0;  Mismatches    1;  Indels  428;  Gaps    3;

Qy          1 CATGGTAGACGGCTGCCCGGAGGGACCACGCGTCTGAGACCGGCGATCGGACCGCCAAAA 60
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Db        110 CATGGTAGACGGCTGCCCGGAGGGACCACGCGTCTGAGACCGGCGATCGGACCGCCAAAA 169

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RESULT 4
BQ885551

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DEFINITION  AGENCOURT_8748027 NIH_MGC_130 Mus musculus cDNA clone IMAGE:6335237
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ACCESSION   BQ885551
VERSION     BQ885551.1  GI:22277569
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 944)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,
            Ph.D.
             cDNA Library Preparation: ResGen, Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13797  row: f  column: 06
            High quality sequence stop: 623.
FEATURES             Location/Qualifiers
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BASE COUNT      184 a    288 c    272 g    200 t
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ORIGIN

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Qy        210 CGAGGCCCCAGGCGCTGGGTGGTGCTGGTGGCAGTGCTGTTCAGCTTCCTCTTGCTCTCC 269
Db        181 CGAGGCCCCAGGCGCTGGGTGGTGCTGGTGGCAGTGCTGTTCAGCTTCCTCTTGCTCTCC 240

Qy        270 CTCATGGCTGGCTTGCTGGTGTGGCACTTCCATTATCGGAATGTGCGGGTTCAAAAAGTC 329
Db        241 CTCATGGCTGGCTTGCTGGTGTGGCACTTCCATTATCGGAATGTGCGGGTTCAAAAAGTC 300

Qy        330 TTCAATGGCCATCTGAGGATCACAAATGAGATCTTTCTGGATGCGTATGAGAACTCCACC 389
Db        301 TTCAATGGCCATCTGAGGATCACAAATGAGATCTTTCTGGATGCGTATGAGAACTCCACC 360

Qy        390 TCCACAGAGTTTATCAGCCTGGCCAGCCAGGTGAAGGAGGCGCTGAAGCTGCTGTACAAT 449
Db        361 TCCACAGAGTTTATCAGCCTGGCCAGCCAGGTGAAGGAGGCGCTGAAGCTGCTGTACAAT 420

Qy        450 GAAGTCCCTGTCCTGGGTCCCTACCACAAGAAGTCGGCTGTAACTGCCTTCAGTGAGGGC 509
Db        421 GAAGTCCCTGTCCTGGGTCCCTACCACAAGAAGTCGGCTGTAACTGCCTTCAGTGAGGGC 480

Qy        510 AGTGTCATCGCCTACTACTGGTCAGAGTTCAGCATCCCCCCACACCTGGCAGAAGAGGTT 569
Db        481 AGTGTCATCGCCTACTACTGGTCAGAGTTCAGCATCCCCCCACACCTGGCAGAAGAGGTT 540

Qy        570 GATCGCGCCATGGCTGTGGAGCGAGTTGTAACATTGCCACCCCGAGCACGGGCACTGAAA 629
Db        541 GATCGCGCCATGGCTGTGGAGCGAGTTGTAACATTGCCACCCCGAGCACGGGCACTGAAA 600

Qy        630 TCCTTCGTGCTAACATCTGTGGTGGCCTTCCCCATTGACCCCAGAATGCTGCAGAGGACT 689
Db        601 TCCTTCGTGCTAACATCTGTGGTGGCCTTCCCCATTGACCCCAGAATGCTGCAGAGGACT 660

Qy        690 CAGGACAACAGCTGCAGTTTTGCCCTGCATGCCCATGGTGCAGCAGTGACACGCTTCACT 749
Db        661 CAGGACAACAGCTGCAGTTTTGCCCTGCATGCCCATGGTGCAGCAGTGACACGCTTCACT 720

Qy        750 ACCCCTGGCTTCCCCAACAGTCCCTACCCGGCGCATGCCCGCTGCCAGTGGGTCCTGCGG 809
Db        721 ACCCCTGGCCTTCCCAACAGTCCCTACCCCGCGCATGCCCGCTGCCAGTGGGTCCTGCGG 780

Qy        810 GGGGACGCCGACTCTGTGCTGAGCCTCACCTTCCGAAGCTTTGATGTCGCTCCCTGTGAT 869
Db        781 GGGGACGCCGACTCTGTGCTGAGCCTCACCTTCCGAACCTTTGATGTCCCTCCCTGTGAT 840

Qy        870 GAGCAT-GGCAGTGACCTGGTCACCGT-GTATGATAGCCTGAGCCCCATGGAACCCCACG 927
Db        841 GACCATGGGCATTGCCCTGGCCCCCGTGGTATGATAACCCTGAGCCCCATGGGACCCCCA 900

Qy        928 CTGTGGTGCGGCTGTGTGG 946
Db        901 CCCTGGTGGTGCGGGCTTG 919
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RESULT 5
BI688367

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LOCUS       BI688367                884 bp    mRNA    linear   EST 18-SEP-2001
DEFINITION  603316692F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5356487 5',
            mRNA sequence.
ACCESSION   BI688367
VERSION     BI688367.1  GI:15650996
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 884)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey Green M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11906  row: h  column: 24
            High quality sequence stop: 831.
FEATURES             Location/Qualifiers
     source          1. .884
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5356487"
                     /sex="female, virgin"
                     /tissue_type="infiltrating ductal carcinoma"
                     /dev_stage="5 months"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Mam6"
                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigator
                     providing samples: Jeffrey Green, M.D., NIH"
BASE COUNT      197 a    232 c    268 g    187 t
ORIGIN
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Query Match 26.8%; Score 833.6; DB 12; Length 884;
Best Local Similarity 98.6%; Pred. No. 2.7e-153;
Matches 872; Conservative 0; Mismatches 9; Indels 3; Gaps 3;

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Qy       1165 GGAATATCAAGGTGCCCAACAACCGGAACGTGAAGGTGCGCTTCAAACTCTTCTATCTGG 1224
Db          1 GGAATATCAAGGTGCCCAACAACCGGAACGTGAAGGTGCGCTTCAAACTCTTCTATCTGG 60

Qy       1225 TGGACCCCAACGTACCAGTGGGCTCCTGCACCAAGGACTATGTGGAGATCAACGGGGAGA 1284
Db         61 TGGACCCCAACGTACCAGTGGGCTCCTGCACCAAGGACTATGTGGAGATCAACGGGGAGA 120

Qy       1285 AGTACTGCGGTGAGAGGTCCCAGTTTGTGGTGAGCAGCAACAGCAGCAAGATTACAGTCC 1344
Db         121 AGTACTGCGGTGAGAGGTCCCAGTTTGTGGTGAGCAGCAACAGCAGCAAGATTACAGTCC 180

Qy       1345 ACTTCCATTCTGATCACTCGTACACGGACACCGGGTTCCTAGCTGAGTACCTCTCCTACG 1404
Db         181 ACTTCCATTCTGATCACTCGTACACGGACACCGGGTTCCTAGCTGAGTACCTCTCCTACG 240

Qy       1405 ACTCCAACGACCCGTGCCCAGGGATGTTCATGTGCAAGACTGGACGGTGCATCCGAAAGG 1464
Db         241 ACTCCAACGACCCGTGCCCAGGGATGTTCATGTGCAAGACTGGACGGTGCATCCGAAAGG 300

Qy       1465 AACTGCGCTGCGACGGCTGGGCAGACTGCCCGGATTATAGTGATGAGCGTTACTGCCGAT 1524
Db         301 AACTGCGCTGCGACGGCTGGGCAGACTGCCCGGATTATAGTGATGAGCGTTACTGCCGAT 360

Qy       1525 GCAATGCCACCCACCAGTTCACGTGCAAAAACCAGTTCTGCAAGCCCCTCTTCTGGGTCT 1584
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Db        361 GCAATGCCACCCACCAGTTCACGTGCAAAAACCAGTTCTGCAAGCCCCTCTTCTGGGTCT 420

Qy       1585 GTGACAGTGTCAACGACTGTGGGGACGGAAGTGACGAGGAGGGCTGCAGCTGTCCTGCTG 1644

Db        421 GTGACAGTGTCAACGACTGTGGGGACGGAAGTGACGAGGAGGGCTGCAGCTGTCCTGCTG 480

Qy       1645 GGAGTTTCAAGTGTTCCAATGGGAAGTGTCTCCCTCAGAGCCAGAAGTGTAATGGGAAGG 1704

Db        481 GGAGTTTCAAGTGTTCCAATGGGAAGTGTCTCCCTCAGAGCCAGAAGTGTAATGGGAAGG 540

Qy       1705 ACAACTGTGGAGATGGGTCTGACGAGGCTTCATGTGACAGCGTGAATGTCGTCTCTTGCA 1764

Db        541 ACAACTGTGGAGATGGGTCTGACGAGGCTTCATGTGACAGCGTGAATGTCGTCTCTTGCA 600

Qy       1765 CCAAATATACCTACCGCTGCCAAAATGGCCTCTGTCTGAG-CAAGGGCAACCCTGAGTGT 1823

Db        601 CCAAATATACCTACCGCTGCCAAAATGGCCTCTGTCTGAGCCAAGGGCAACCCTGAGTGT 660

Qy       1824 GATGGGAAGACGGACTGTAGCGATGGCTCCGATGAGAAAAACTGTGACTGTGGGCTGCGA 1883

Db        661 GATGGGAAGACGGACTGTAGCGATGGCTCCGATGAGAAAAACTGTGACTGTGGGCTGCGA 720

Qy       1884 TCCTTTACCAAACAGGCTCGCG-TGGTTGGTGGCACGAATGCGGACGAGGGCGAGTGGCC 1942

Db        721 TCCTTTACCAGACAGGCTCGCGTTGGTTGGTGGCACGAATGCGGACGAGGGCGAGTGGCC 780

Qy       1943 CTGGCAGGTGAGCCTCCACGCCCTGGGCCAGGGCCACTTGTGTGGGGCCTCGC-TCATCT 2001

Db        781 CTGGCAGGTGAGCCTCCAAGCCCTGGGGCCAGGCCACTTGTGTGGGGGCTCGCTTCATCT 840

Qy       2002 CTCCTGACTGGCTGGTCTCTGCAGCTCATTGCTTTCAGGATGAC 2045

Db        841 CTCCTGACTGGCTGGTCTCTGCAGCTCATCGCTTCCAGGATGCC 884
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RESULT 6
BI690615

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LOCUS       BI690615                803 bp    mRNA    linear   EST 18-SEP-2001
DEFINITION  603314210F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5354067 5',
            mRNA sequence.
ACCESSION   BI690615
VERSION     BI690615.1  GI:15653244
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 803)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey Green M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11900  row: d  column: 04
            High quality sequence stop: 755.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5354067"
                     /sex="female, virgin"
                     /tissue_type="infiltrating ductal carcinoma"
                     /dev_stage="5 months"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Mam6"
                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigator
                     providing samples: Jeffrey Green, M.D., NIH"
BASE COUNT      170 a    259 c    200 g    174 t
ORIGIN
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Query Match 25.4%; Score 788.8; DB 12; Length 803;
Best Local Similarity 99.6%; Pred. No. 1.7e-144;
Matches 801; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Qy        654 GCCTTCCCCATTGACCCCAGAATGCTGCAGAGGACTCAGGACAACAGCTGCAGTTTTGCC 713

Db          1 GCCTTCCCCATTGACCCCAGAATGCTGCAGAGGACTCAGGACAACAGCTGCAGTTTTGCC 60

Qy        714 CTGCATGCCCATGGTGCAGCAGTGACACGCTTCACTACCCCTGGCTTCCCCAACAGTCCC 773

Db         61 CTGCATGCCCATGGTGCAGCAGTGACACGCTTCACTACCCCTGGCTTCCCCAACAGTCCC 120

Qy        774 TACCCGGCGCATGCCCGCTGCCAGTGGGTCCTGCGGGGGGACGCCGACTCTGTGCTGAGC 833

Db        121 TACCCGGCGCATGCCCGCTGCCAGTGGGTCCTGCGGGGGGACGCCGACTCTGTGCTGAGC 180

Qy        834 CTCACCTTCCGAAGCTTTGATGTCGCTCCCTGTGATGAGCATGGCAGTGACCTGGTCACC 893

Db        181 CTCACCTTCCGAAGCTTTGATGTCGCTCCCTGTGATGAGCATGGCAGTGACCTGGTCACC 240

Qy        894 GTGTATGATAGCCTGAGCCCCATGGAACCCCACGCTGTGGTGCGGCTGTGTGGCACCTTC 953

Db        241 GTGTATGATAGCCTGAGCCCCATGGAACCCCACGCTGTGGTGCGGCTGTGTGGCACCTTC 300

Qy        954 TCACCCTCCTACAACCTGACTTTCCTCTCCTCCCAGAACGTCTTCCTTGTCACGCTGATA 1013

Db        301 TCACCCTCCTACAACCTGACTTTCCTCTCCTCCCAGAACGTCTTCCTTGTCACGCTGATA 360

Qy       1014 ACCAATACTGACCGGCGACATCCTGGCTTTGAGGCCACTTTCTTCCAGCTGCCCAAGATG 1073

Db        361 ACCAATACTGACCGGCGACATCCTGGCTTTGAGGCCACTTTCTTCCAGCTGCCCAAGATG 420

Qy       1074 AGCAGCTGTGGCGGCTTTTTGAGTGACACCCAAGGGACATTTAGCAGCCCCTACTATCCA 1133

Db        421 AGCAGCTGTGGCGGCTTTTTGAGTGACACCCAAGGGACATTTAGCAGCCCCTACTATCCA 480

Qy       1134 GGCCACTACCCGCCCAACATCAACTGCACATGGAATATCAAGGTGCCCAACAACCGGAAC 1193

Db        481 GGCCACTACCCGCCCAACATCAACTGCACATGGAATATCAAGGTGCCCAACAACCGGAAC 540

Qy       1194 GTGAAGGTGCGCTTCAAACTCTTCTATCTGGTGGACCCCAACGTACCAGTGGGCTCCTGC 1253

Db        541 GTGAAGGTGCGCTTCAAACTCTTCTATCTGGTGGACCCCAACGTACCAGTGGGCTCCTGC 600

Qy       1254 ACCAAGGACTATGTGGAGATCAACGGGGAGAAGTACTGCGGTGAGAGGTCCCAGTTTGTG 1313

Db        601 ACCAAGGACTATGTGGAGATCAACGGGGAGAAGTACTGCGGTGAGAGGTCCCAGTTTGTG 660

Qy       1314 GTGAGCAGCAACAGCAGCAAGATTACAGTCCACTTCCATTCTGATCACTCGTACACGGAC 1373

Db        661 GTGAGCAGCAACAGCAGCAAGATTACAGTCCACTTCCATTCTGATCACTCGTACACGGAC 720

Qy       1374 ACCGGGTTCCTAGCTGAGTACCTCTCCTACGACTCCAACGACCCGTGCCCAGGGATGTTC 1433

Db        721 ACCGGGTTCCTAGCTGAGTACCTCTCCTACGACTCCAACGACCCGTGCCCAGGGATTGTC 780

Qy       1434 ATGTGCAAGACTGGACGGTGCATC 1457

Db        781 ATGTGCAAGA-TGGACGGTGCATC 803
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RESULT 7
BQ951529

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LOCUS       BQ951529                990 bp    mRNA    linear   EST 21-AUG-2002
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DEFINITION  AGENCOURT_8952916 NCI_CGAP_Co24 Mus musculus cDNA clone
            IMAGE:6475074 5', mRNA sequence.
ACCESSION   BQ951529
VERSION     BQ951529.1  GI:22367007
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: The Cepko Laboratory
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM14013  row: d  column: 19
            High quality sequence stop: 635.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6475074"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Co24"
                     /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.6 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      229 a    272 c    286 g    201 t      2 others
ORIGIN

  Query Match           25.1%;  Score 778.2;  DB 13;  Length 990;
  Best Local Similarity  92.9%;  Pred. No. 1.9e-142;
  Matches  924;  Conservative    0;  Mismatches   60;  Indels   11;  Gaps   10;

Qy        981 TCCTCCCAGAACGTCTTCCTTGTCACGCTGATAACCAATACTGACCGGCGACATCCTGGC 1040
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Db          1 TCCTCCCAGAACGTCTTCCTTGTCACGCTGATAACCAATACTGACCGGCGACATCCTGGC 60

Qy       1041 TTTGAGGCCACTTTCTTCCAGCTGCCCAAGATGAGCAGCTGTGGCGGCTTTTTGAGTGAC 1100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTTGAGGCCACTTTCTTCCAGCTGCCCAAGATGAGCAGCTGTGGCGGCTTTTTGAGTGAC 120

Qy       1101 ACCCAAGGGACATTTAGCAGCCCCTACTATCCAGGCCACTACCCGCCCAACATCAACTGC 1160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCCAAGGGACATTTAGCAGCCCCTACTATCCAGGCCACTACCCGCCCAACATCAACTGC 180

Qy       1161 ACATGGAATATCAAGGTGCCCAACAACCGGAACGTGAAGGTGCGCTTCAAACTCTTCTAT 1220
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Db        181 ACATGGAATATCAAGGTGCCCAACAACCGGAACGTGAAGGTGCGCTTCAAACTCTTCTAT 240

Qy       1221 CTGGTGGACCCCAACGTACCAGTGGGCTCCTGCACCAAGGACTATGTGGAGATCAACGGG 1280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGGTGGACCCCAACGTACCAGTGGGCTCCTGCACCAAGGACTATGTGGAGATCAACGGG 300

Qy       1281 GAGAAGTACTGCGGTGAGAGGTCCCAGTTTGTGGTGAGCAGCAACAGCAGCAAGATTACA 1340
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Db        301 GAGAAGTACTGCGGTGAGAGGTCCCAGTTTGTGGTGAGCAGCAACAGCAGCAAGATTACA 360

Qy       1341 GTCCACTTCCATTCTGATCACTCGTACACGGACACCGGGTTCCTAGCTGAGTACCTCTCC 1400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCCACTTCCATTCTGATCACTCGTACACGGACACCGGGTTCCTAGCTGAGTACCTCTCC 420

Qy       1401 TACGACTCCAACGACCCGTGCCCAGGGATGTTCATGTGCAAGACTGGACGGTGCATCCGA 1460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TACGACTCCAACGACCCGTGCCCAGGGATGTTCATGTGCAAGACTGGACGGTGCATCCGA 480

Qy       1461 AAGGAACTGCGCTGCGACGGCTGGGCAGACTGCCCGGATTATAGTGATGAGCGTTACTGC 1520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AAGGAACTGCGCTGCGACGGCTGGGCAGACTGCCCGGATTATAGTGATGAGCGTTACTGC 540

Qy       1521 CGATGCAATGCCACCCACCAGTTCACGTGCAAAAACCAGTTCTGCAAGCCCCT-CTTCTG 1579
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Db        541 CGATGCAATGCCACCCACCAGTTCACGTGCAAAAACCAGTTCTGCAAGCCCCTCCTTCTG 600

Qy       1580 GGTCTGTGACAGTGTCAACGACT-GTGGGGACGGAAGTGACGAGGAGGGCTGCAGCTGTC 1638
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Db        601 GGTCTGTGACAGTGTCAACGACTGGTGGGGACGGAAGTGACGAGGAGGGCTGCAGCTGTC 660

Qy       1639 CTGCTGGGAGTTTCAAGTGTTCCAATGGGAAGTGTCTCCCTCAGAGCCAGAAGT-GTAAT 1697
              |||||||||||||||||||| ||||||||||||||||||||||||||||||| |||||
Db        661 CTGCTGGGAGTTTCAAGTGTCCCAATGGGAAGTGTCTCCCTCAGAGCCAGAAGTGGTAAT 720

Qy       1698 GGGAAGGACAACTGT--GGAGATGGGTCTGACGAGGCTTCATGTG-ACAGCGTGAATGTC 1754
              |||||||| |||| ||||||||||||||||||||||||||||| ||||||||||||||
Db        721 GGGAAGGACNCCTGTTGGGAGATGGGTCTGACGAGGCTTCATGTGAACAGCGTGAATGTC 780

Qy       1755 GTCTCTTGCACCAAATATACCTACCGCTGCCAAAATGGCCTCTGTCTGAGCAAGGGCAAC 1814
              |||||||||||| |||||||||||||||| |||||||| |||||||||||| |||||| |
Db        781 GTCTCTTGCACC-AATATACCTACCGCTGGCAAAATGG-CTCTGTCTGAGC-AGGGCACC 837

Qy       1815 CCTGAGTGTGATGGGAAGACGGACTGTAGCGATGGCTCCGATGAGAAAAACTGTGACTGT 1874
              | ||| || |||||||||||||||||| |||||| |||||||| |||||| | || |||
Db        838 CTTGATTGGGATGGGAAGACGGACTGTACCGATGG-TCCGATGAAAAAAAC-GGGAATGT 895

Qy       1875 GGGCTGCGATCCTTTACCAAACAGGCTCGCGTGGTTGGTGGCACGAATGCGGACGAGGGC 1934
              |||||| || |||| | |||       | |       | | |       | || ||||
Db        896 GGGCTGGGACCCTTACCAAAAGGCTTCCCGGGTTGGTGGGCAAGCNCCCCCAACAAGGGG 955

Qy       1935 GAGTGGCCCTGGCAGGTGAGCCTCCACGCCCTGGG 1969
              || ||||| |   | | | |  | || ||  ||
Db        956 CAGGGGCCCCGTGGAGGGGGACCTCCCGGCCGTGG 990


RESULT 8
BG919617
LOCUS       BG919617                762 bp    mRNA    linear   EST 05-JUN-2001
DEFINITION  602823173F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4951962 5',
            mRNA sequence.
ACCESSION   BG919617
VERSION     BG919617.1  GI:14300093
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey Green M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10909  row: a  column: 19
            High quality sequence stop: 727.
FEATURES             Location/Qualifiers
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                     /strain="FVB/N"
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                     /clone="IMAGE:4951962"
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                     /clone_lib="NCI_CGAP_Mam6"
                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigator
                     providing samples: Jeffrey Green, M.D., NIH"
BASE COUNT      164 a    243 c    190 g    165 t
ORIGIN

  Query Match             24.5%;  Score 760.4;  DB 12;  Length 762;
  Best Local Similarity   99.9%;  Pred. No. 6.4e-139;
  Matches  761;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        682 AGAGGACTCAGGACAACAGCTGCAGTTTTGCCCTGCATGCCCATGGTGCAGCAGTGACAC 741
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGAGGACTCAGGACAACAGCTGCAGTTTTGCCCTGCATGCCCATGGTGCAGCAGTGACAC 60

Qy        742 GCTTCACTACCCCTGGCTTCCCCAACAGTCCCTACCCGGCGCATGCCCGCTGCCAGTGGG 801
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Db         61 GCTTCACTACCCCTGGCTTCCCCAACAGTCCCTACCCGGCGCATGCCCGCTGCCAGTGGG 120

Qy        802 TCCTGCGGGGGGGACGCCGACTCTGTGCTGAGCCTCACCTTCCGAAGCTTTGATGTCGCTC 861
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Db        121 TCCTGCGGGGGGACGCCGACTCTGTGCTGAGCCTCACCTTCCGAAGCTTTGATGTCGCTC 180

Qy        862 CCTGTGATGAGCATGGCAGTGACCTGGTCACCGTGTATGATAGCCTGAGCCCCATGGAAC 921
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Db        181 CCTGTGATGAGCATGGCAGTGACCTGGTCACCGTGTATGATAGCCTGAGCCCCATGGAAC 240

Qy        922 CCCACGCTGTGGTGCGGCTGTGTGGCACCTTCTCACCCTCCTACAACCTGACTTTCCTCT 981
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Db        241 CCCACGCTGTGGTGCGGCTGTGTGGCACCTTCTCACCCTCCTACAACCTGACTTTCCTCT 300

Qy        982 CCTCCCAGAACGTCTTCCTTGTCACGCTGATAACCAATACTGACCGGCGACATCCTGGCT 1041
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Db        301 CCTCCCAGAACGTCTTCCTTGTCACGCTGATAACCAATACTGACCGGCGACATCCTGGCT 360

Qy       1042 TTGAGGCCACTTTCTTCCAGCTGCCCAAGATGAGCAGCTGTGGCGGCTTTTTGAGTGACA 1101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTGAGGCCACTTTCTTCCAGCTGCCCAAGATGAGCAGCTGTGGCGGCTTTTTGAGTGACA 420

Qy       1102 CCCAAGGGACATTTAGCAGCCCCTACTATCCAGGCCACTACCCGCCCAACATCAACTGCA 1161
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCCAAGGGACATTTAGCAGCCCCTACTATCCAGGCCACTACCCGCCCAACATCAACTGCA 480

Qy       1162 CATGGAATATCAAGGTGCCCAACAACCGGAACGTGAAGGTGCGCTTCAAACTCTTCTATC 1221
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CATGGAATATCAAGGTGCCCAACAACCGGAACGTGAAGGTGCGCTTCAAACTCTTCTATC 540

Qy       1222 TGGTGGACCCCAACGTACCAGTGGGCTCCTGCACCAAGGACTATGTGGAGATCAACGGGG 1281
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGGTGGACCCCAACGTACCAGTGGGCTCCTGCACCAAGGACTATGTGGAGATCAACGGGG 600

Qy       1282 AGAAGTACTGCGGTGAGAGGTCCCAGTTTGTGGTGAGCAGCAACAGCAGCAAGATTACAG 1341
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGAAGTACTGCGGTGAGAGGTCCCAGTTTGTGGTGAGCAGCAACAGCAGCAAGATTACAG 660

Qy       1342 TCCACTTCCATTCTGATCACTCGTACACGGACACCGGGTTCCTAGCTGAGTACCTCTCCT 1401
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TCCACTTCCATTCTGATCACTCGTACACGGACACCGGGTTCCTAGCTGAGTACCTCTCCT 720

Qy       1402 ACGACTCCAACGACCCGTGCCCAGGGATGTTCATGTGCAAGA 1443
              |||||||||| ||||||||||||||||||||||||||||||
Db        721 ACGACTCCAAAGACCCGTGCCCAGGGATGTTCATGTGCAAGA 762


RESULT 9
CB208872
LOCUS       CB208872                874 bp    mRNA    linear   EST 16-MAY-2003
DEFINITION  AGENCOURT_11350695 NIH_MGC_164 Mus musculus cDNA clone
            IMAGE:30241011 5', mRNA sequence.
ACCESSION   CB208872
VERSION     CB208872.2  GI:29133712
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 874)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     On Feb 4, 2003 this sequence version replaced gi:28250435.
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. David Rowe and Dr. Mina
             cDNA Library Preparation: Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM0308  row: g  column: 04
            High quality sequence stop: 655.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:30241011"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_164"
                     /note="Vector: pCMV-SPORT6.1.ccdb; Site_1: EcoRV; Site_2:
                     NotI; Non-normalized full-length enriched library from
                     pooled mouse embryonic limb, maxilla and mandible, day
                     10.5 and 11.5 (size selected for the 0.5-1 kb fragments)
                     Cloned directionally, priming method: Oligo-dT.  cDNA
                     enrichment: >1k bp, Average insert size 1.8k bp. Priming
                     sequence: 5'GACTAGTTCTAGATCGCGAGCGGCCGCCC(T) 3'. Tissue
                     contributed by, David Rowe. Library constructed by ResGen,
                     Invitrogen Corp."
BASE COUNT      193 a    230 c    260 g    190 t      1 others
ORIGIN

  Query Match             24.4%;  Score 759.4;  DB 14;  Length 874;
  Best Local Similarity   98.9%;  Pred. No. 9.8e-139;
  Matches  785;  Conservative    0;  Mismatches    7;  Indels    2;  Gaps    2;

Qy       1387 CTGAGTACCTCTCCTACGACTCCAACGACCCGTGCCCAGGGATGTTCATGTGCAAGACTG 1446
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTGAGTACCTCTCCTACGACTCCAACGACCCGTGCCCAGGGATGTTCATGTGCAAGACTG 60

Qy       1447 GACGGTGCATCCGAAAGGAACTGCGCTGCGACGGCTGGGCAGACTGCCCGGATTATAGTG 1506
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACGGTGCATCCGAAAGGAACTGCGCTGCGACGGCTGGGCAGACTGCCCGGATTATAGTG 120

Qy       1507 ATGAGCGTTACTGCCGATGCAATGCCACCCACCAGTTCACGTGCAAAAACCAGTTCTGCA 1566
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATGAGCGTTACTGCCGATGCAATGCCACCCACCAGTTCACGTGCAAAAACCAGTTCTGCA 180

Qy       1567 AGCCCCTCTTCTGGGTCTGTGACAGTGTCAACGACTGTGGGGACGGAAGTGACGAGGAGG 1626
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGCCCCTCTTCTGGGTCTGTGACAGTGTCAACGACTGTGGGGACGGAAGTGACGAGGAGG 240

Qy       1627 GCTGCAGCTGTCCTGCTGGGAGTTTCAAGTGTTCCAATGGGAAGTGTCTCCCTCAGAGCC 1686
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Db        241 GCTGCAGCTGTCCTGCTGGGAGTTTCAAGTGTTCCAATGGGAAGTGTCTCCCTCAGAGCC 300

Qy       1687 AGAAGTGTAATGGGAAGGACAACTGTGGAGATGGGTCTGACGAGGCTTCATGTGACAGCG 1746
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Qy       1747 TGAATGTCGTCTCTTGCACCAAATATACCTACCGCTGCCAAAATGGCCTCTGTCTGAGCA 1806
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Db        361 TGAATGTCGTCTCTTGCACCAAATATACCTACCGCTGCCAAAATGGCCTCTGTCTGAGCA 420

Qy       1807 AGGGCAACCCTGAGTGTGATGGGAAGACGGACTGTAGCGATGGCTCCGATGAGAAAAACT 1866
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Db        421 AGGGCAACCCTGAGTGTGATGGGAAGACGGACTGTAGCGATGGCTCCGATGAGAAAAACT 480

Qy       1867 GTGACTGTGGGCTGCGATCCTTTACCAAACAGGCTCGCGTGGTTGGTGGCACGAATGCGG 1926
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Db        481 GTGACTGTGGGCTGCGATCCTTTACCAAACAGGCTCGCGTGGTTGGTGGCACGAATGCGG 540

Qy       1927 ACGAGGGCGAGTGGCCCTGGCAGGTGAGCCTCCACGCCCTGGGCCAGGGCCACTTGTGTG 1986
             |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        541 ACGAGGGCGAGTGGCCCTGGCAGGTGAGCCTCCACGCCCTGNGCCAGGGCCACTTGTGTG 600

Qy       1987 GGGCCTCGCTCATCTCTCCTGACTGGCTGGTCTCTGCAGCTCATTGCTTTCAGGATGACA 2046
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Db        601 GGGCCTCGCTCATCTCTCCTGACTGGCTGGTCTCTGCAGCTCATTGCTTTCAGGATGACA 660

Qy       2047 AAAATTTCAAGTACTCAGACTACACGATGTGGACGGCCTTCCTGGGTCTGCTGGACCAGA 2106
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Db        661 AAAATTTCAAGTACTCAGACTACACGATGTGGACGGCCTTCCTGGGTCTGCTGGACC-GA 719

Qy       2107 GCAAGCGCAGTGCCTCTGGGGTGCAGGAGCTGAAGCTCAAACGTATCAT-CACCCACCCT 2165
             |||||||||||||||||||||||||||||||| |||| ||||||||| | ||||||| |
Db        720 GCAAGCGCAGTGCCTCTGGGGTGCAGGAGCTGAAACTCATACGTATCATCCGCCCACCGT 779

Qy       2166 TCCTTCAATGATTT 2179
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Db        780 TCCTTCAATGGATT 793
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RESULT 10
BI664081

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LOCUS       BI664081                798 bp    mRNA    linear   EST 12-SEP-2001
DEFINITION  603289385F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5323485 5',
            mRNA sequence.
ACCESSION   BI664081
VERSION     BI664081.1  GI:15578314
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 798)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey Green M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11820  row: i  column: 22
            High quality sequence stop: 771.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /strain="FVB/N"
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                     /clone="IMAGE:5323485"
                     /sex="female, virgin"
                     /tissue_type="infiltrating ductal carcinoma"
                     /dev_stage="5 months"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Mam6"
                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigator
                     providing samples: Jeffrey Green, M.D., NIH"
BASE COUNT      167 a    223 c    240 g    168 t
ORIGIN
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  Query Match             24.1%;  Score 747.2;  DB 12;  Length 798;
  Best Local Similarity   98.6%;  Pred. No. 2.5e-136;
  Matches  785;  Conservative    0;  Mismatches    8;  Indels    3;  Gaps    3;

Qy         16 CCCGGAGGGACCACGCGTCTGAGACCGGCGATCGGACCGCCAAAACCATGGGTAGCAATC 75
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Db          1 CCCGGAGGGACCACGCGTCTGAGACCGGCGATCGGACCGCCAAAACCATGGGTAGCAATC 60

Qy         76 GGGGCCGCAAGGCCGGAGGGGGCTCTCAGGACTTCGGCGCGGGACTCAAGTACAACTCCC 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGGGCCGCAAGGCCGGAGGGGGCTCTCAGGACTTCGGCGCGGGACTCAAGTACAACTCCC 120

Qy        136 GGCTAGAGAACATGAATGGCTTTGAGGAGGGTGTGGAGTTCCTGCCTGCGAACAATGCCA 195
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Db        121 GGCTAGAGAACATGAATGGCTTTGAGGAGGGTGTGGAGTTCCTGCCTGCGAACAATGCCA 180

Qy        196 AGAAAGTGGAGAAGCGAGGCCCCAGGCGCTGGGTGGTGCTGGTGGCAGTGCTGTTCAGCT 255
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Db        181 AGAAAGTGGAGAAGCGAGGCCCCAGGCGCTGGGTGGTGCTGGTGGCAGTGCTGTTCAGCT 240

Qy        256 TCCTCTTGCTCTCCCTCATGGCTGGCTTGCTGGTGTGGCACTTCCATTATCGGAATGTGC 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCTCTTGCTCTCCCTCATGGCTGGCTTGCTGGTGTGGCACTTCCATTATCGGAATGTGC 300

Qy        316 GGGTTCAAAAAGTCTTCAATGGCCATCTGAGGATCACAAATGAGATCTTTCTGGATGCGT 375
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Db        301 GGGTTCAAAAAGTCTTCAATGGCCATCTGAGGATCACAAATGAGATCTTTCTGGATGCGT 360

Qy        376 ATGAGAACTCCACCTCCACAGAGTTTATCAGCCTGGCCAGCCAGGTGAAGGAGGCGCTGA 435
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Db        361 ATGAGAACTCCACCTCCACAGAGTTTATCAGCCTGGCCAGCCAGGTGAAGGAGGCGCTGA 420

Qy        436 AGCTGCTGTACAATGAAGTCCCTGTCCTGGGTCCCTACCACAAGAAGTCGGCTGTAACTG 495
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Db        421 AGCTGCTGTACAATGAAGTCCCTGTCCTGGGTCCCTACCACAAGAAGTCGGCTGTAACTG 480

Qy        496 CCTTCAGTGAGGGCAGTGTCATCGCCTACTACTGGTCAGAGTTCAGCATCCCCCCACACC 555
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Db        481 CCTTCAGTGAGGGCAGTGTCATCGCCTACTACTGGTCAGAGTTCAGCATCCCCCCACACC 540

Qy        556 TGGCAGAAGAGGTTGATCGCGCCATGGCTGTGGAGCGAGTTGTAACATTGCCACCCCGAG 615
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Db        541 TGGCAGAAGAGGTTGATCGCGCCATGGCTGTGGAGCGAGTTGTAACATTGCCACCCCGAG 600

Qy        616 CACGGGCACTGAAATCCTTCGTGCTAACATCTGTGGTGGCCTTCCCCATTGACCCCAGAA 675
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Db        601 CACGGGCACTGAAATCCTTCGTGCTAACATCTGTGGTGGCCTTCCCCATTGAGCCCAGAA 660

Qy        676 TGCTGCAGAGGACTCAGGACAACAGCTGCAGTTTTGCCCTGCATG-CCCATGGTGCAGCA 734
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Db        661 TGCTGCAGAGGACTCAGGACAACAGCTGCAGTTTTGCCCTGCATGCCCCATGGTGCAGCA 720

Qy        735 GTG-ACACGCTTCACTACCCCTGGCTTCCCCAACAGTCCCTACCCGGCGCATGCCCGCTG 793
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Db        721 GTGAACACGCTTCAGTACCCCTGGGTT-CCCAACAGTCCCTACCCGGGGCATTGCCGTTG 779

Qy        794 CCAGTGGGTCCTGCGG 809
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Db        780 GCAGTGGGTCCTGCGG 795
```

RESULT 11
BY756896

```
LOCUS       BY756896                746 bp    mRNA    linear   EST 17-DEC-2002
DEFINITION  BY756896 RIKEN full-length enriched, blastocyst Mus musculus cDNA
            clone I1C0035F06 3', mRNA sequence.
ACCESSION   BY756896
```

VERSION BY756896.1 GI:27190109
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 746)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani;K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
MEDLINE 22354683
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES Location/Qualifiers
source 1. .746
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/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="I1C0035F06"
/dev_stage="blastocyst"
/clone_lib="RIKEN full-length enriched, blastocyst"
BASE COUNT 172 a 193 c 224 g 155 t 2 others
ORIGIN

Query Match 23.8%; Score 739.2; DB 14; Length 746;
Best Local Similarity 99.3%; Pred. No. 9.3e-135;
Matches 741; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy       2343 CTGATCCTGCAGAAGGGTGAGATCCGTGTCATCAACCAGACCACCTGTGAGGACCTCATG 2402
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Db          1 CTGATCNTGCAGNAAGGTGAGATCCGTGTCATCAACCAGACCACCTGTGAGACCCTCATG 60

Qy       2403 CCGCAGCAGATCACCCCACGAATGATGTGTGTGGGTTTCCTCAGTGGGGGTGTGGACTCC 2462
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Qy       2523 GCTGGTGTGGTGAGCTGGGGTGAAGGCTGCGCTCAGAGGAACAAGCCAGGCGTGTACACA 2582
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Qy       2583 AGGCTCCCTGTAGTTCGGGACTGGATCAAAGAGCACACTGGGGTATAGCAGCATGGACAG 2642
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Qy       2643 ACAGCCGACCACAAACACCCACAGGGATGCCCGACATGCACACCTGGATACAGGAGAGGA 2702
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Db        301 ACAGCCGACCACAAACACCCACAGGGATGCCCGACATGCACACCTGGATACAGGAGAGGA 360

Qy       2703 ACACTGACGACATTTATGCTGTGGCCTCCCCCCCCCCAACACAACCCAGACTGTGAACTGC 2762
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Qy       2823 GCGTGCTAGCGGCCCAGCCTGGGGGCAAGGGTTTGATGGCAGCCTTCCCCCTCTAGCCCT 2882
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Db        601 GAGCCCTATGGGAGGAGGGGCTCAGGGTCACTCTTTTCAGGAAGCGCCAGCCCTAGGAAC 660

Qy       3003 CCCAGAAAAGAGTGGTACCTAAGGCTGAAATTGTTTTGCTGTTGCCAGGGGTGGGTATTT 3062
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCCAGAAAAGAGTGGTACCTAAGGCTGAAATTGTTTTGCTGTTGCCAGGGGTGGGTATTT 720

Qy       3063 GAGAGTAAAACATTTTATTTCTTTTT 3088
             |||||||||||||||||||||||||||
Db        721 GAGAGTAAAACATTTTATTTCTTTTT 746
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RESULT 12
BI416218
LOCUS BI416218 846 bp mRNA linear EST 14-AUG-2001
DEFINITION 602989878F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5145762 5',

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            mRNA sequence.
ACCESSION   BI416218
VERSION     BI416218.1  GI:15177141
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 846)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by:Incyte Genomics, Inc.
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11359  row: l  column: 19
            High quality sequence start: 20
            High quality sequence stop: 793.
FEATURES             Location/Qualifiers
     source          1. .846
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="CZECH II"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5145762"
                     /tissue_type="pooled lung tumors"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NCI_CGAP_Lu33"
                     /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; Site_1: NotI; Site_2: EcoRI; 1st
                     strand cDNA was prepared from mRNA obtained from pooled
                     lung tumors with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCTGTTTTTTTTTTTTTTTT 3']. 
                     Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not
                     I and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      178 a    224 c    262 g    182 t
ORIGIN

  Query Match             23.8%;  Score 739.2;  DB 12;  Length 846;
  Best Local Similarity   97.1%;  Pred. No. 9e-135;
  Matches  816;  Conservative    0;  Mismatches   18;  Indels    6;  Gaps    6;

Qy       1687 AGAAGTGTAATGGGAAGGACAACTGTGGAGATGGGTCTGACGAGGCTTCATGTGACAGCG 1746
             |||   | |   | |  |   |||||||||||||||||||||||||||||||||||||||
Db          1 AGATCCGCACGAGTAGAGGACACTGTGGAGATGGGTCTGACGAGGCTTCATGTGACAGCG 60

Qy       1747 TGAATGTCGTCTCTTGCACCAAATATACCTACCGCTGCCAAAATGGCCTCTGTCTGAGCA 1806
             |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db         61 TGAATGTCGTCTCTTGCACCAAATATACCTACCGCTGCCAAAATGGGCTCTGTCTGAGCA 120

Qy       1807 AGGGCAACCCTGAGTGTGATGGGAAGACGGACTGTAGCGATGGCTCCGATGAGAAAAACT 1866
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGGGCAACCCTGAGTGTGATGGGAAGACGGACTGTAGCGATGGCTCCGATGAGAAAAACT 180

Qy       1867 GTGACTGTGGGCTGCGATCCTTTACCAAACAGGCTCGCGTGGTTGGTGGCACGAATGCGG 1926
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGACTGTGGGCTGCGATCCTTTACCAAACAGGCTCGCGTGGTTGGTGGCACGAATGCGG 240

Qy       1927 ACGAGGGCGAGTGGCCCTGGCAGGTGAGCCTCCACGCCCTGGGCCAGGGCCACTTGTGTG 1986
             |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db        241 ACGAGGGCGAGTGGCCCTGGCAGGTGAGCCTCCACGCCCTGGGCCA-GGCCACTTGTGTG 299

Qy       1987 GGGCCTCGCTCATCTCTCCTGACTGGCTGGTCTCTGCAGCTCATTGCTTTCAGGATGACA 2046
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 GGGCCTCGCTCATCTCTCCTGACTGGCTGGTCTCTGCAGCTCATTGCTTTCAGGATGACA 359

Qy       2047 AAAATTTCAAGTACTCAGACTACACGATGTGGACGGCCTTCCTGGGTCTGCTGGACCAGA 2106
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 AAAATTTCAAGTACTCAGACTACACGATGTGGACGGCCTTCCTGGGTCTGCTGGACCAGA 419

Qy       2107 GCAAGCGCAGTGCCTCTGGGGTGCAGGAGCTGAAGCTCAAACGTATCATCACCCACCCTT 2166
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 GCAAGCGCAGTGCCTCTGGGGTGCAGGAGCTGAAGCTCAAACGTATCATCACCCACCCTT 479

Qy       2167 CCTTCAATGATTTCACCTTCGACTATGACATCGCCTTGCTGGAGCTGGAGAAGTCGGTGG 2226
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 CCTTCAATGATTTCACCTTCGACTATGACATCGCCTTGCTGGAGCTGGAGAAGTCGGTGG 539

Qy       2227 AGTACAGCACCGTCGTGCGCCCCATCTGCCTGCCTGATGCTACCCATGTCTTCCCTGCTG 2286
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 AGTACAGCACCGTCGTGCGCCCCATCTGCCTGCCTGATGCTACCCATGTCTTCCCTGCTG 599

Qy       2287 GC-AAGGCCATCTGGGTCACAGGCTGGGGGCACACAAAAGAGGGAGGT-ACCGGAGCGCT 2344
             || ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        600 GCAAAGGCCATCTGGGTCACAGGCTGGGGGCACACAAAAGAGGGAGGTCACCGGAGCGCT 659

Qy       2345 GATCCTGCAGAAGGGTGAGATCCGTGTCATC-AACCAGACCACCTGTGAGGACCTCATGC 2403
             |||||||||||||||||||||||||||||||| ||||||||| ||||||||||||||||
Db        660 GATCCTGCAGAAGGGTGAGATCCGTGTCATCAAACCAGACCGACTGTGAGGACCTCATGC 719

Qy       2404 CGCAGCAGATCACCCCACGAATGATGTGTGTGGGTTTCCTCAGTGGGGGTGTGGACTCCT 2463
             ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        720 CGCAG-AGATCACCCCACGAATGATGTGTGTGGGTTTCCTCAGTGGGGGTGTGGACTCCT 778

Qy       2464 GCCAGGGTGACTCTGGTGGCCCCCTTGTCAAGCGCGGAGAAAGATGGGCGAATGTTCCAGG 2523
             | |||||||||||||||||||||||||||||||| ||||| ||||||||||||||||
Db        779 G-CAGGGTGACTCTGGTGGCCCCCTTGTCAAGCGCGGAGCAAGATTGGCGAATGTTCCAGG 837


RESULT 13
BF301347
LOCUS       BF301347                1116 bp    mRNA    linear   EST 21-NOV-2000
DEFINITION  602029796F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4165103 5',
            mRNA sequence.
ACCESSION   BF301347
VERSION     BF301347.1  GI:11247870
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1116)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9451  row: o  column: 24
            High quality sequence stop: 686.
FEATURES             Location/Qualifiers
     source          1. .1116
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4165103"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_SG2"
                     /note="Organ: salivary gland; Vector: pCMV-SPORT6; Site_1:
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NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 325 a 315 c 302 g 174 t
ORIGIN

Query Match 23.7%; Score 735.8; DB 10; Length 1116;
Best Local Similarity 92.1%; Pred. No. 3.9e-134;
Matches 800; Conservative 0; Mismatches 62; Indels 7; Gaps 2;

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Qy       1137 CACTACCCGCCCAACATCAACTGCACATGGAATATCAAGGTGCCCAACAACCGGAACGTG 1196
Db             1 CACTACCCGCCCAACATCAACTGCACATGGAATATCAAGGTGCCCAACAACCGGAACGTG 60

Qy       1197 AAGGTGCGCTTCAAACTCTTCTATCTGGTGGACCCCAACGTACCAGTGGGCTCCTGCACC 1256
Db            61 AAGGTGCGCTTCAAACTCTTCTATCTGGTGGACCCCAACGTACCAGTGGGCTCCTGCACC 120

Qy       1257 AAGGACTATGTGGAGATCAACGGGGAGAAGTACTGCGGTGAGAGGTCCCAGTTTGTGGTG 1316
Db            121 AAGGACTATGTGGAGATCAACGGGGAGAAGTACTGCGGTGAGAGGTCCCAGTTTGTGGTG 180

Qy       1317 AGCAGCAACAGCAGCAAGATTACAGTCCACTTCCATTCTGATCACTCGTACACGGACACC 1376
Db            181 AGCAGCAACAGCAGCAAGATTACAGTCCACTTCCATTCTGATCACTCGTACACGGACACC 240

Qy       1377 GGGTTCCTAGCTGAGTACCTCTCCTACGACTCCAACGACCCGTGCCCAGGGATGTTCATG 1436
Db            241 GGGTTCCTAGCTGAGTACCTCTCCTACGACTCCAACGACCCGTGCCCAGGGATGTTCATG 300

Qy       1437 TGCAAGACTGGACGGTGCATCCGAAAGGAACTGCGCTGCGACGGCTGGGCAGACTGCCCG 1496
Db            301 TGCAAGACTGGACGGTGCATCCGAAAGGAACTGCGCTGCGACGGCTGGGCAGACTGACCG 360

Qy       1497 GATTATAGTGATGAGCGTTACTGCCGATGCAATGCCACCCACCAGTTCACGTGCAAAAAC 1556
Db            361 GATTATAGTGATGAGCGTTACTGCCGATGCAATGCCACCCACCAGTTCACGTGCAAAAAC 420

Qy       1557 CAGTTCTGCAAGCCCCTCTTCTGGGTCTGTGACAGTGTCAACGACTGTGGGGACGGAAGT 1616
Db            421 CAGTTCTGCAAGCCCCTCTTCTGGGTCTGTGACAGTGTCAACGACTGTGGGGACGGAAGT 480

Qy       1617 GACGAGGAGGGCTGCAGCTGTCCTGCTGGGAGTTTCAAGTGTTCCAATGGGAAGTGTCTC 1676
Db            481 GACGAGGAGGGCTGCAGCTGTCCTGCTGGGAGTTTCAAGTGTTCCAATGGGAAGTGTCTC 540

Qy       1677 CCTCAGAGCCAGAAGTGTAATGGGAAGGACAACTGTGGAGATGGGTCTGACGAGGCTTCA 1736
Db            541 CCTCAGAGCCAGAAGTGTACTGGGAAGGACAACTGTGGAGATGGGTCTGACGAGGCTTCA 600

Qy       1737 TGTGACAGCGTGAATGTCGTCTCTTGCACCAAATATACCTACCGCTGCCAAAATGGCCTC 1796
Db            601 TGTGACAGCGTGAATGTCGTCTCTTGCACCAGATATACCTACCGATGCCAAAAAGGCCTC 660

Qy       1797 TGTCTGAGCAAGGGCAACCCTGAGTGTGATGGGAAGACGGACTGTAGCGATGGCTCCGAT 1856
Db            661 TGTCTGAGCAAGGGCCACCCTGAGTGTGAGGGGAAGACCGACTGTACGAATGGCTCCGCA 720

Qy       1857 G---AGAAAAACTGTGACTGTGGGCTGCGATCCTTTACCAAACAGGCTCGCGTGGTTGGT 1913
Db            721 GGACAAACACACTGGGACTGTGGGCAGCGATCCTTTACCAAACAGGATCAGGTGACAGGT 780

Qy       1914 GGCACGAATGCG----GACGAGGGCGAGTGGCCCTGGCAGGTGAGCCTCCACGCCCTGGG 1969
Db            781 GGGAACGAATTGCAGACAAAGGGACAAAGTGCCCGTGCACGAGAGCCTCCACGGCCTGTA 840

Qy       1970 CCAGGGCCACTTGTGTGGGGCCTCGCTCA 1998
Db            841 GAACAGGCCAATGAGTGGAACCCCTAGCA 869
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RESULT 14
BI646380

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LOCUS       BI646380                786 bp    mRNA    linear   EST 12-SEP-2001
DEFINITION  603276244F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5316539 5',
            mRNA sequence.
ACCESSION   BI646380
VERSION     BI646380.1  GI:15560616
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 786)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11802  row: h  column: 12
            High quality sequence stop: 764.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:10090"
                     /clone="IMAGE:5316539"
                     /tissue_type="tumor, gross tissue"
                     /dev_stage="10 months"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Mam3"
                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigators
                     providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
                     Reference for transgenic model: Xu et al., Nature Genetics
                     22, 37-43 (1999)."
BASE COUNT      177 a    203 c    235 g    171 t
ORIGIN
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Query Match 23.6%; Score 732; DB 12; Length 786;
Best Local Similarity 98.7%; Pred. No. 2.4e-133;
Matches 780; Conservative 0; Mismatches 5; Indels 5; Gaps 4;

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Qy       1409 CAACGACCCGTGCCCAGGGATGTTCATGTGCAAGACTGGACGGTGCATCCGAAAGGAACT 1468
Db             1 CAACGACCCGTGCCCA-GGATGTTCATGTGCAAGACTGGACGGTGCATCCGAAAGGAACT 59

Qy       1469 GCGCTGCGACGGCTGGGCAGACTGCCCGGATTATAGTGATGAGCGTTACTGCCGATGCAA 1528
Db            60 GCGCTGCGACGGCTGGGCAGACTGCCCGGATTATAGTGATGAGCGTTACTGCCGATGCAA 119

Qy       1529 TGCCACCCACCAGTTCACGTGCAAAAACCAGTTCTGCAAGCCCCTCTTCTGGGTCTGTGA 1588
Db           120 TGCCACCCACCAGTTCACGTGCAAAAACCAGTTCTGCAAGCCCCTCTTCTGGGTCTGTGA 179

Qy       1589 CAGTGTCAACGACTGTGGGGACGGAAGTGACGAGGAGGGCTGCAGCTGTCCTGCTGGGAG 1648
Db           180 CAGTGTCAACGACTGTGGGGACGGAAGTGACGAGGAGGGCTGCAGCTGTCCTGCTGGGAG 239

Qy       1649 TTTCAAGTGTTCCAATGGGAAGTGTCTCCCTCAGAGCCAGAAGTGTAATGGGAAGGACAA 1708
Db           240 TTTCAAGTGTTCCAATGGGAAGTGTCTCCCTCAGAGCCAGAAGTGTAATGGGAAGGACAA 299

Qy       1709 CTGTGGAGATGGGTCTGACGAGGCTTCATGTGACAGCGTGAATGTCGTCTCTTGCACCAA 1768
Db           300 CTGTGGAGATGGGTCTGACGAGGCTTCATGTGACAGCGTGAATGTCGTCTCTTGCACCAA 359
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Qy       1769 ATATACCTACCGCTGCCAAAATGGCCTCTGTCTGAGCAAGGGCAACCCTGAGTGTGATGG 1828
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Db        360 ATATACCTACCGCTGCCAAAATGGCCTCTGTCTGAGCAAGGGCAACCCTGAGTGTGATGG 419

Qy       1829 GAAGACGGACTGTAGCGATGGCTCCGATGAGAAAAACTGTGACTGTGGGCTGCGATCCTT 1888
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 GAAGACGGACTGTAGCGATGGCTCCGATGAGAAAAACTGTGACTGTGGGCTGCGATCCTT 479

Qy       1889 TACCAAACAGGCTCGCGTGGTTGGTGGCACGAATGCGGACGAGGGCGAGTGGCCCTGGCA 1948
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 TACCAAACAGGCTCGCGTGGTTGGTGGCACGAATGCGGACGAGGGCGAGTGGCCCTGGCA 539

Qy       1949 GGTGAGCCTCCACGCCCTGGGCCAGGGCCACTTGTGTGGGGCCTCGCTCATCTCTCCTGA 2008
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 GGTGAGCCTCCACGCCCTGGGGCCAGGCCACTTGTGTGGGGCCTCGCTCATCTCTCCTGA 599

Qy       2009 CTGGCTGGTCTCTGCAGCTCATTGCTTTCAGGATGACAAAAATTTCAAGTACTCAGACTA 2068
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 CTGGCTGGTCTCTGCAGCTCATTGCTTTCAGGATGACAAAAATTTCAAGTACTCAGACTA 659

Qy       2069 CACG-ATGTGGACGGCCTTCCTGGGTCTGCTGGACCAGAGCAAGCGCAGTGCCTCTGGGG 2127
             |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 CACGAATGTGGACGGCCTTCCTGGGTCTGCTGGACCAGAGCAAGCGCAGTGCCTCTGGGG 719

Qy       2128 TGCAGGAGCTGAAGCTCAAACGTATCATCACCCACCCTTCCTTCAATGATTTCACCTTCG 2187
             ||||||||||||||||||||||||||||||  |||  | |||||||||  ||||||||||
Db        720 TGCAGGAGCTGAAGCTCAAACGTATCATCACCAACC--TTCTTCAATGA-TTCACCTTCG 776

Qy       2188 ACTATGACAT 2197
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Db        777 ACTATGACAT 786


RESULT 15
BG915045
LOCUS       BG915045                 928 bp    mRNA    linear   EST 05-JUN-2001
DEFINITION  602814325F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:4936590 5',
            mRNA sequence.
ACCESSION   BG915045
VERSION     BG915045.1  GI:14295521
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 928)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
            Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10869  row: a  column: 07
            High quality sequence stop: 793.
FEATURES             Location/Qualifiers
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                     /strain="NMRI"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4936590"
                     /tissue_type="tumor, gross tissue"
                     /dev_stage="5 months"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Mam4"
                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigators
                     providing samples: Lothar Hennighausen/Priscilla Furth,
                     NIH Reference for transgenic model: Li et al., Cell Growth
                     and  Differentiation 7, 3-11 (1996)."
BASE COUNT      216 a    258 c    273 g    181 t
ORIGIN

  Query Match           23.2%;  Score 721;  DB 12;  Length 928;
  Best Local Similarity   93.2%;  Pred. No. 3.3e-131;
  Matches  832;  Conservative    0;  Mismatches   50;  Indels   11;  Gaps    7;

Qy       1886 CTTTACCAAACAGGCTCGCGTGGTTGGTGGCACGAATGCGGACGAGGGCGAGTGGCCCTG 1945
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTTTACCAAACAGGCTCGCGTGGTTGGTGGCACGAATGCGGACGAGGGCGAGTGGCCCTG 60

Qy       1946 GCAGGTGAGCCTCCACGCCCTGGGCCAGGGCCACTTGTGTGGGGCCTCGCTCATCTCTCC 2005
             |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db         61 GCAGGTGAGCCTCCACGCCCTGGGCCA-GGCCACTTGTGTGGGGCCTCGCTCATCTCTCC 119

Qy       2006 TGACTGGCTGGTCTCTGCAGCTCATTGCTTTCAGGATGACAAAAATTTCAAGTACTCAGA 2065
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 TGACTGGCTGGTCTCTGCAGCTCATTGCTTTCAGGATGACAAAAATTTCAAGTACTCAGA 179

Qy       2066 CTACACGATGTGGACGGCCTTCCTGGGTCTGCTGGACCAGAGCAAGCGCAGTGCCTCTGG 2125
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 CTACACGATGTGGACGGCCTTCCTGGGTCTGCTGGACCAGAGCAAGCGCAGTGCCTCTGG 239

Qy       2126 GGTGCAGGAGCTGAAGCTCAAACGTATCATCACCCACCCTTCCTTCAATGATTTCACCTT 2185
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 GGTGCAGGAGCTGAAGCTCAAACGTATCATCACCCACCCTTCCTTCAATGATTTCACCTT 299

Qy       2186 CGACTATGACATCGCCTTGCTGGAGCTGGAGAAGTCGGTGGAGTACAGCACCGTCGTGCG 2245
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Db        300 CGACTATGACATCGCCTTGCTGGAGCTGGAGAAGTCGGTGGAGTACAGCACCGTCGTGCG 359

Qy       2246 CCCCATCTGCCTGCCTGATGCTACCCATGTCTTCCCTGCTGGCAAGGCCATCTGGGTCAC 2305
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Db        360 CCCCATCTGCCTGCCTGATGCTACCCATGTCTTCCCTGCTGGCAAGGCCATCTGGGTCAC 419

Qy       2306 AGGCTGGGGGCACACAAAAGAGGGAGGTACCGGAGCGCTGATCCTGCAGAAGGGTGAGAT 2365
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 AGGCTGGGGGCACACAAAAGAGGGAGGTACCGGAGCGCTGATCCTGCAGAAGGGTGAGAT 479

Qy       2366 CCGTGTCATCAACCAGACCACCTGTGAGGACCTCATGCCGCAGCAGATCACCCCACGAAT 2425
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 CCGTGTCATCAACCAGACCACCTGTGAGGACCTCATGCCGCAGCAGATCACCCCACGAAT 539

Qy       2426 GATGTGTGTGGGTTTCCTCAGTGGGGGTGTGGACTCCTGCCAGGGTGACTCTGGT--GGC 2483
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||  | |
Db        540 GATGTGTGTGGGTTTCCTCAGTGGGGGTGTGGACTCCTGCCAGGGTGACTCTGGTTGGCC 599

Qy       2484 CCCTTGTCAAGCGCGGAGAAAGATGGGCGAATGTTCCAGGCTGGTGTGGTGAGCTGGGGT 2543
             || |   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 CCTTGTCAAAGCGCGGAGAAAGATGGGCGAATGTTCCAGGCTGGTGTGGTGAGCTGGGGT 659

Qy       2544 GAAGGCTGCGCTCAGAGGAACAAG-CCAGGCGTGTACA-CAAGGCTCCCTGTAGTTCGGG 2601
             |||||||||||||||||||||||||| |||||||||||| |||| ||||||||||||||||
Db        660 GAAGGCTGCGCTCAGAGGAACAAGCCCAGGCGTGTACACCAAGGGTCCCTGTAGTTCGGG 719

Qy       2602 ACTGGATCAAAGAGCACACTGGGGTATAGCAGCATGGA-CAGACAGCCGACCACAAACAC 2660
             | |   |||| ||||||||||||||||||||||||| |||||||       ||||||
Db        720 AACTGGATCAAGAACACACTGGGGTATAGCAGCATGGACCAGACAGCGACAACAAAACAC 779

Qy       2661 CCACAGGGATGCCCGACATGCACACCTGGAT---ACAGGAGAGGAACACTGACGACATTT 2717
             |||||||||||||| ||||||||||||||   |   |   | | ||||||||||||
Db        780 CCACAGGGATGCCCGAAATGCACACCTGGATTACAGGAGCAGGAACCACTGACGACATCA 839

Qy       2718 ATGCTGTGGCCTCCCCCCCCCAACACAACCCAGACTGTGAACTGCATCCTTAG 2770
             |||||| ||| |||||  | |  | |  ||||||||||   ||| ||
Db        840 TGCTTGTGGCATCCACCCCC--AAAACAACACAACTGTGAACTGGTACCTAAG 890
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Search completed: February 21, 2004, 07:12:09
Job time : 6230 secs